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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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SUMMARIES

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AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AX512287
Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U.,	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1	Homo sapiens	Homo sapiens (human)	,	AX512287.1 GI:23392631	AX512287	43 from Patent W002053742.	AX512287 1102 bp DNA linear PAT 27-SEP-2002	

ALIGNMENTS

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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A.,
Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A.,
Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U.,
Rothenberg,M., Stone,D., Boldog,F., Shenoy,S. and Anderson,D.
Proteins and nucleic acids encoding same
Patent: WO 02053/42.A 45 11-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
1. 1102
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                 841 GITTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGGAGCAGGTGATGGGTTCAGAG
                                                                                                                                                                              GCATTCCTGGATTCTGCCAGAATCCTTTTGAGGCCCTTGTCCCCATATATCAGTAGGAGTC
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; Pred. No. 2.6e-164;
0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 74.0%; Score 815.6; DB 6; Length 2457; Best Local Similarity 99.5%; Pred. No. 3.1e-119; Matches 818; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Qy 124 CCGTACTGCGGGGCCCTGAGCCCTCGGCCGCATCATGGGGGGGCTCAAACGCGCAGCCG 183	2y 184 GGCACCTGGCCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCC 243	Qy 244 CICALGGCCCCTCCTGGGTCCTCTCGCTGCTCTGTTTCATGACGAATGGGACGTTG 303	QY 304 GAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGCCCCTGGAC 363 Db 286 GAGCCCGCGGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGCCCCTGGAC 345	QY 364 GEOGGGGGACACCCCCCCCCCCTCGTGGTGCCGGCCAACTACAGCCAAGTGGAG 423 Db 346 GGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAG 405	QY 424 CIDGGCGCCGACCTGGCGCCTGGCGCTCACCCGCCTGGCCTG	Qy	QY 544 ACCGGTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAA 603 Db 526 ACCGGTGGGGAGACGTCCAGGAGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAA 585	QY 604 GIGGAGCTGAGGCTGCTGGGCGAGCCACCTGTCATGTCTCTACAGCCGGGTCCC 663 Db 586 GIGGAGCTAAGGCTGCTGGGGCGACCTGTCATCATGTCTCTACAGCCGGGTCCC 645	Qy 664 THCAACCTCACTCTCCAGAIATTGCCAGGGAIGCTGTGTGCTGGCTACCCAGAGGGCGC 723	Qy 724 AGGGACACCTGCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAGGCGGCGGCTGG 783 10 11 <td< th=""><th>QY 784 TTCCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGAAACCGCCCTGGAGTT 843 Db 766 TTCCAGGCAGGAATCACCAGCTTTGGCTTTGGCTGTGGACGGAGAAACCGCCCTGGAGTT 825 QY 844 TTCACTGCTGTGCTACCTATGAGGATACGGGAGCAGGTGATGGGTTCAGAGCCT 903 Db 826 TTCACTGCTGTGGCTACCTATGAGGATGGATACGGGAGCAGGTGATGGGTTCAGAGCCT 885</th><th>Qy 904 GGGCCTGCCTTTCCCACCCCAGAAGACCCCAGTCAGAT 945</th><th>RESULT 4 AX480935 LOCUS LOCUS DEFINITION Sequence 31 from Patent W00246383. ACCESSION AX480935.1 GI:22217574 VERSION AX480935.1 GI:22217574 SOURCE Homo sapiens (human)</th></td<>	QY 784 TTCCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGAAACCGCCCTGGAGTT 843 Db 766 TTCCAGGCAGGAATCACCAGCTTTGGCTTTGGCTGTGGACGGAGAAACCGCCCTGGAGTT 825 QY 844 TTCACTGCTGTGCTACCTATGAGGATACGGGAGCAGGTGATGGGTTCAGAGCCT 903 Db 826 TTCACTGCTGTGGCTACCTATGAGGATGGATACGGGAGCAGGTGATGGGTTCAGAGCCT 885	Qy 904 GGGCCTGCCTTTCCCACCCCAGAAGACCCCAGTCAGAT 945	RESULT 4 AX480935 LOCUS LOCUS DEFINITION Sequence 31 from Patent W00246383. ACCESSION AX480935.1 GI:22217574 VERSION AX480935.1 GI:22217574 SOURCE Homo sapiens (human)
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PAT 18-SEP-2002

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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
               TTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGGTTCAGAGCCT
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Primates, Catarrhini, Hominidae, Homo.
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Yue, H., Azimzai, Y., Kallick, D.A., Baughn, M.R., Griffin, J.A., Swarnakar, A., Lal, P.G., Walia, N.K., Hafalia, A.J., Gandhi, A.R., Au-Young, J., Elliott, V.S., Rankumar, J., Thangavelu, K., Lu, Y., Warren, B.A., Lu, D.A., Lee, E.A., Tribouley, C.M., Arvizu, C., Delegane, A.M., Yao, M.G., Khan, F.A. and Sanjanwala, M.M. Procein modification and maintenance molecules
Parent: WO 0246383-A 31 13-JUN-2002;
Incyte Genomics, Inc. (US)
Location Qualifiers
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Best Local Similarity 99.5%; Pred. No. 3e-119;
Matches 818; Conservative 0; Mismatches 4
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Homo sapiens
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Bconomy, Trade and Industry of Japan, Louna Lary-Construction: Research Association for Biotechnology; CDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA 5'- & 3'-end one pass sequencing and chone selection: Helix Research Institute (supported by Japan Key Tiran, American etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLQBVELALIGEATCQCLYSQPGPFNLTLQIIPGMLCAGYPEGRRDTCĞGDSGGPLVC
EGGRWFQAGTTSFGFGCGRRNRPQYFTAVATYBANTRAQVMSEPGPAFPTQPSKTQ
SDPQEPREBNCTTLEPECGRAPRPGAMPWBAQVMVPGSRPCHGALVSSWVLAPASCF
LDPNSSDSPPRDLDAMRVLLPSRPRARRVARLVQHBNASWDNASDLALIQLRTPVILS
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AVPLPGDPPHALCPAYQEKEEVGSCWNDSRWSLLCQEEGTWFLAGIRDFPSGCLRPRA
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PQGHQVSRLVISIRLPQHLGIRPPILALLELSSRVEPSPSALPICLHPAGIPPGASCWV
LGWKEPQDRVDVAAAVSILTQRICDCLYQGILPPGTLCVLYAEGQENRCEMTSAPPLL
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VELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPW
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/clone_lib="PLACE1"
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2 (bases I to 2810)

Direct Submission

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(8-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/650
PD 22-JAN-2002
PP 77-JUL-2000 JP 2000253172
PI TOSHIKO TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI SHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
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Primer for synthesizing full-length cDNA and use thereof FH K
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PI YURI KAMAL,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Primer for synthesizing full-length cDNA and use thereof.
BD125219
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002017375-A/650.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity
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ACCESSION
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KEYWORDS
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BD125219
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
CTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAAGTGGA
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Regulation of human prostasin-like serine protease
Patent: WO 0198467-A 1 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
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Pred. No. 7e-75;
0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.8%;
Matches 536; Conservative
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Homo sapiens
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ACCESSION
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AX342934/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                             organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                Length 670;
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Regulation of human prostasin-like serine protease
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                                                                                                                                                                                                                                                                                             Score 472.8; DB 6
Pred. No. 4.9e-65;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 3 from Patent W00198467.
AX342936
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JP 2002017375-A/1916
22-JAN-2002
7-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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DN 22-JANA -2002

PD 22-JANA -2002

PP 07-JUL-2000

PP 07-JUL-2000

PP 1 CSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI ISHII, MATAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINCHI KOJIMA,

BI TETSUJI OTSUKI, HISASHI KOGA

PC CIZNIS/09, CO7K14/47, CO7K16/18, CIZNI/15, CIZNI/19, CIZNI/21, CIZNS/ PC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 670)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                   CGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGCTGGAGCC
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JP 2002017375-A/1916.
Homo sapiens (human)
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DOE Joint Genome Institute, Stanford Human Genome Center and
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1 (bases 1 to 127769)
DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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Homo sapiens chromosome 16 clone RPI1-388M20, complete sequence.
AC009088
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Submitted (03-AUG-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 127769)
DOE Joint Genome Institute.
Direct Submission
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 WO 0198467-A 3 27-DEC-2001;
                                           1. .456
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
              Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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DOE Joint Genome Institute.
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Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
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                                                                                                                                                                                                                          Submitted (199-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 29, 2003 this sequence version replaced gi:29029216.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This insert is not the entire sequence of the clone (entire sequence is 233.4kb). It is clipped at the overlap with AC135050. The number of bases overlapped is 2575.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195476)
DOB Joint Genome Institute.
                                                        Institute, 2800 Mitchell
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                                              Submitted (18-WAR-2003) DOE Joint Genome Institute, 2800 Mitc Drive, Walnut Creek, CA 94598, USA 5 (Dases I to 127769) DOE Joint Genome Institute, Stanford Human Genome Center and Alamos National Laboratory.
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Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
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HTG: HTGS_PHASB1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HTGMC sapiens (human)
Homo sapiens
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Unpublished
2 (bases 1 to 195476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone="RP11-388M20"
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Alamos National Laboratory
Direct Submission
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Best Local Similarity 98.9%;
Matches 282; Conservative
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TITLE JOURNAL AUTHORS

COMMENT

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27404 AGGATGGGACGCTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAG 27463
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.8e-35;
0; Mismatches 3; Indels 0; 0
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                                                                                                      /chromosome="16"
/clone="CTD-2551B20"
/clone_lib="CalTech human BAC library D"
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0; Mismatches 401;
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Millennium Predictive Medicine, Inc. (US)
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Consensus quality: 18238 bases at least Q30
Consensus quality: 188095 bases at least Q30
Consensus quality: 188095 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; garcose-fp estimation
Quality coverage: 6.7 in Q20 bases; garcose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                     Direct Submission
Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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150436: gap of unknown length
195476: contig of 45040 bp in length.
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J., Neckernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: j Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536453. Location/Qualifiers
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/translation="MAQKGVLGPGQLGAVAILLYLGLLRSGTGAEGAEAPCGVAPQAR
ITGGSSAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKBAYEVKLGA
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduco,Q.L., Masiello,C., Maskeri,B., Matrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory Consultanty Arrayed by: The I.M.A.G.E. Consortium (ILNL) CDNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
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On Aug 19, 2003 this sequence version replaced gi:12655206
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/clone lib="NIH MGC_21"
/lab_host="DH10B-R"
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|protein_id="AAH01462.1"
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/db_xref="taxon:9606"
/clone="MGC:2133 IMAGE:3138532"
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/note="synonym: PROSTASIN"
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Web site: http://www.nisc.nih.gov/
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Contact: MGC help desk
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Klauener, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Identification, assessment, prevention, and therapy of
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Millennium Predictive Medicine, Inc.
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Search completed: February 25, 2004, 10:31:04 Job time : 4339 secs

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Aba94396 Human pro
Abq86175 Novel hum
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Abs67730 DNA encod
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Abk12241 cDNA enco Abn95716 Gene #221	Humar	Aas01366 Recombina	4	Aas74051 DNA encod		4	LΩ	Aac87796 Activatio	Aaf55268 Nucleotid	Aac87795 Activatio		Aah78206 Nucleotid	Abn85393 Human NOV	Aaz34034 Human EST	Aac78495 Human EST	Aac58237 Human EST	Acd42567 Novel hum	Aca63602 Novel hum	Aca71766 Human sec	Abx92406 Human PRO
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ABK1224	AAC7781	AASO	ABA9	AAS7405	ABS5643	ABNB	ABN8	AAC8	AAF5	AACB	AAFS	AAH7	ABN8	AAZ3	AAC7	AAC5823	ACD4	ACA6	ACA7	ABX924
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ALIGNMENTS

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Human, NOVX; neurological disorder; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous sclarosis; ancer; immune disorder; allergy;

KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

KW endometriosis; incontinence; psoriasis; soleroderma; alopecia; ulcer;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW metabolic pathway regulation disorder; oytostatic; neuroprotective;

KW metabolic pathway regulation disorder; oytostatic; neuroprotective;

KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

KW dermatological; oxoliferation; motility; haematopoiesis; wound healing;

KW anglogenesis; forensic biology; transgenic animal; drug screening;

KW gene therapy; NOV14a; prostatin precursor-like; chromosome 16; gene; des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Product= "NOV14a"
note= "No stop codon given in the specification"
                                                                                                                                                Human prostatin precursor-like NOV14a DNA, SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                     ABQ93901 standard; DNA; 1102 BP.
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08-JAN-2001; 2001US-0260360P.
28-FEB-2001; 2001US-0272411P.
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02-MAR-2001; 2001US-0272817P.
05-JUL-2001; 2001US-0303231P.
12-JUL-2001; 2001US-0305060P.
10-SEF-2001; 2001US-0318405F.
12-SEP-2001; 2001US-0318700P.
                   (CURA-) CURAGEN CORP
             04-JAN-2002;
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The invention relates to 24 novel human proteins designated NOVI-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ9302). NOVX proteins and collectively retainent, diagnosis or prevention of NOVX-associated disorders or in the manufacture of a medicament for treating such disorders with specific applications described for each of the 24 sociated disorders or in the manufacture of a medicament for treating such disorders are associated with NOVX proteins including neurological disorders (e.g., Allzheimer's, Huntingón's and Parkinson's diseases), chain, behavioural disorders, addiction, tubercous sclerosis, cancers (e.g., allzegies and autoimmune diseases), immune disorders (e.g., hypertension), reproductive disorders, endometriosis, glomerular endochableses, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, glomerular endochableses, thyroiditis, cardiovascular disease (cirrhosis, glomerular endochableses), cardiovascular disease (disorders, obesity, bacterial infections and particularly cardiowyopathy, clincothinence, psoriasis, scleroderma, alogecia, uccers, panoreatitis, disbectes, cirrhosis, glomerular endothablesis, polycystic kidney disease, endocrinc disorders, obesity, bacterial infections and particularly cardiowyopathy, clincothinence, psoriasis, scleroderma, alogecia, uccers, panoreaticism, cell signal processing-related disorders and disorders of metabolic pathway regulation. NOVX nucleic acids and polyceptides may confidentification of small molecules that modulate or inhibit processes such care useful as a source of primers or probes for forensic proteins and cloning NOVX homologues in other cell types (comprising NOVX nucleic acids and elementer proteins and cloning NOVX homologues in other cell types. Cells cartivity of NOVX proteins and for identifying and cloning not identify Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders. ij S, Anderson D; Tchernev VT, Liu X, Spytek KA; Lepley DM, Burgess CE, Vernet CAM, iore P, Ellerman K, Malyankar U, Length 1102; Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other; WM, Lepley DM, Burgess CE, Sciore P, Ellerman K, Maly Boldog F, Gloo X, Shenoy J, Miller CE, Eisen A, ; Score 1102; DB 6; ; Pred. No. 8.2e-185; 0; Mismatches 0; Claim 9a; Page 142; 323pp; English Query Match 100.0%; Best Local Similarity 100.0%; Matches 1102; Conservative 0 Alsobrook JP, 7 n M, Grosse WM, Edinger S, Scio g M, Stone D, Bo M, Taupier RJ, 1 WPI; 2002-583619/62 P-PSDB; ABB09523. Rothenberg M, Patturajan M, Gorman L, Edi Padigaru M,

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Gaps

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Indels

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GGGCCCTTGTCCTGGGCCATGGCCCAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGCT

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01-NOV-2002

Human prostatin precursor-like NOV14b DNA, SEQ ID NO:45. (first entry)

polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy; atherosclerosis; cell signal processing-related disorder; atherosclerosis; cell signal processing-related disorder; ametabolic pathway regulation disorder; cytostatic; neuroprotective; antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic; dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis; differentiation; proliferation motility; haematopoiesis; wound healing; angiogenesis; forensic biology; transgenic animal; drug screening; gene therapy; NOV14b; prostatin precursor-like; gene; ds. Human; NOVX; neurological disorder; Alzheimer's disease; huttington's disease; parkinson's disease; pain, behavioural disorder; addiction; tuberous sclerosis; cancer; immune disorder; allergy; autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes; thyroiditis; cardiovascular disease; hypertension; reproductive disorder; endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer; pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

Homo sapiens

Location/Qualifiers 1. .18 /*tag= b /product= "NOV14b" 1093. .1102 /*tag= c /*tag= a 19..1092 Key 5'UTR 3'UTR CDS

WO200253742-A2

07-JAN-2002; 2002WO-US000375

08-JAN-2001; 2001US-0260360P. 28-FEB-2001; 2001US-0272411P. 02-MAR-2001; 2001US-0272411P. 05-JUL-2001; 2001US-0303231P. 12-JUL-2001; 2001US-030305060P. 10-SEP-2001; 2001US-0318406P. 2002US-00037417 05-JAN-2001; 04-JAN-2002;

(CURA-) CURAGEN CORP

Guo X, Shenoy S, Anderson , Eisen A; Spytek KA; JE, Vernet CAM, Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA Patturajan M, Grosse WM, Lepley DM, Burgess CE, Verne Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, An Padigaru M, Taupier RJ, Miller CE, Eisen A;

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WPI; 2002-583619/62.

P-PSDB; ABB09524

receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders. Novel polypeptides and nucleic acids homologous to transmembrane

Claim 9a; Page 143; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX-associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24

NOVX proteins, based on their homology to known proteins. Various disorders are associated with NOVX proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tuberous sclerosis, cancers (e.g., allergies and autoimmune diseases), myasthenia gravis, asthmatic (e.g., allergies and autoimmune diseases), myasthenia gravis, asthmatic various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, cirrhosis, glomerular endotheliosis, alopecia, ulcers, pancreatitis, cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing related disorders and disorders of metabolic pathway regulation. NoVX nucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which binds to a NOVX protein, and are also useful as a targets for the cidentification of small molecules that modulate or inhibit processes such as neurogenesis, cell differentiation, cell motility, cellular complete and sequences can be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic biology and for identifying and cloning NOVX homologues in other cell types. Cells comparising NOVX nowled are useful for producing non-human comminishers of the comparishment of study for studying the function and for interior and for it farms and more cell trypes. Cells 480 CCCCCGTACTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAG 180 CCCCCGTACTGCGGGGGCGCCCTTGGGCCCGCATCGTGGGGGGGTCAAACGCGCAA 180 TCCCTCATCGCCCCCTCCTGGGTCCTCTCGCTGCTCATGTTCATGACGAATGGGACG 300 rresaeccesescearesresresracresrescereserecresceres 360 420 420 480 GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAG 600 9 activity of NOVX proteins and for identifying and evaluating modulators of NOVX activity. The present sequence represents DNA encoding the 1 GGGCCCTTGTCCTGGGCCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGGCCTGGGGGCT 1 ececcerrerectacecearceceaseaseseserectacecercesecasecreceeeeeee COGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC CCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC TCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGATGGGACG TTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCTG GACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG GACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG GAGCTGGGCCCCGGCCCTGCTGCGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCC gaderregedecegacerregedecerregedecerregedentalegedes adecregedes GTGTGGCCTGTCTGCCTGCCCCCCCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGG Gaps . 0 Length 1102; Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other; Indels 2; DB 6; 8.2e-185; ·, 0; Mismatches 100.0%; Score 1102; 100.0%; Pred. No. 8. prostatin precursor-like protein NOV14b Matches 1102; Conservative Local Similarity 19 61 121 181 181 241 361 421 481 541 541 121 241 301 301 361 421 481 Query Match g qq à à 엄 à g à 셤 à 셤 ð d ð 원 à 셤 ò

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                          CCCTTCAACCTCACTCCCAGATATTGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGC
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Nucleic acids encoding novel human proteases, useful for useful for

Caenepeel

Manning G,

Sudarsanam S,

Whyte D,

Charydczak G;

Plowman G,

WPI; 2002-139913/18

P-PSDB; AAU82753

26-JUN-2000; 2000US-0214047P

(SUGE-) SUGEN INC

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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are card the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. theumatoid arthritis and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, hypotenosion, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections such as ocular disease (e.g. virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. ABX31744-ABX31802 represent DNA sequences encoding for the novel human proteases of the invention
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                            and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
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Pred. No. 1.6e-134;
0; Mismatches 4;
                                                                                                                             Claim 26; Fig 18S-TT; 313pp; English.
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Best Local Similarity 99.5%;
Matches 818; Conservative
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anticonvulsant; neuroprotective; nootropic; cytostatic; antipporiatic;

anticonvulsant; neuroprotective; antidiabetic; antiparkinsonian;

anticamemic; antifilammatory; anticuloer; antianginal; cardiant;

Mampatetrial; fungicide; gastrointesthnal; antidiarrheic; laxative;

A namibacterial; fungicide; gastrointesthnal; antidiarrheic; laxative;

A namibacterial; fungicide; gastrointesthnal; antidiarrheic; laxative;

A namibacterial; antidiarreriosclerofic; mypotensive; vasotropic;

antitumour; antirheumatic; immunosuppressive; antiallergic; antithyroid;

M ephrotropic; antigout; hypromimetic; antiarhritic; uropathic;

ophthalmological; antidepressant; neuroleptic; antiinfertility;

auditory; antiseborrheic; antidepressant; neuroleptic; antiinfertility;

anthelmintic; proteozoacide; crohn's disease; hypertension; autoimmune;

millammatory; anaemia; cell proliferative; developmental; epithelial;

scabies; neurological; Alzheimer's disease; reproductive;

w ectopic pregnancy; gene therapy; vaccine; disorder; prostasin; gene; ss.

    .2457
    /*tag= a
    /product= "protein modification and maintenance molecule"

                                                                                903
                                                                                                          Swarnakar A;
Elliott VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.
                                          766 TTCCAGGCAGGAATCACCAGCTTTGGCTTTGGCTGTGGACGGAGAAACCGCCCTGGAGTT
                                                                                TTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCT
  TTCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAGAAACCGCCCTGGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PMMM; protein modification and maintenance molecule;
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                                                                                                                                                                                         GGGCCTGCCTTTCCCACCCAGCCCCAGAAGACCCAGTCAGAT 927
                                                                                                                                                               GGGCCTGCCTTTCCCACCCCAGCCCCAGAGACCCCAGTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                Human PMMM encoding sequence Incyte ID 2751509CB1.
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Lal PG, Walia NK, Hafalia AJA, Gandhi AR, Au-
Ramkumar J, Thangavelu K, Iu Y, Warren BA, Li
Tribouley CM, Arvizu C, Delegeane AM, Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                         ABQ75956 standard; cDNA; 2681
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21-DEC-2000; 2000US-0257603P.
05-JAN-2001; 2001US-0260110P.
19-JAN-2001; 2001US-0264629P.
25-JAN-2001; 2001US-0264623P.
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                                                                                                                                                                                                                                                                   RESULT 4
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The invention relates to an isolated Protein Modification and Maintenance (PMM) polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. proliferative disorders, developmental disorders, epithelial disorders proliferative disorders (e.g. Alzahenko, autoimmune/inflammatory disorders, epithelial disorders reproductive disorders (e.g. Alzahenko, as disease) reproductive disorders (e.g. Catopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 CCAGGAGCCTTCCAGGACTCAGCTCTCAGTCCTACCCAGGAAGAACCTGAAGATCTGGAC 142
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                               Score 806.6; DB 4;
Pred. No. 6.2e-133;
0; Mismatches 74;
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2000JP-00183765.
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[1 Similarity 92.0%;
862; Conservative
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02-MAY-2000;
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Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss. note= "No start or stop codons shown" *tag= a product= "Prostasin-like enzyme" partial Location/Qualifiers complement (3. .536) Homo sapiens

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WO200198467-A2

27-DEC-2001

22-JUN-2001; 2001WO-EP007117.

23-JUN-2000; 2000US-0213588P. 20-MAR-2001; 2001US-0276909P.

(FARB) BAYER AG.

Morozov V; Kiao Y,

WPI; 2002-114576/15. P-PSDB; AAU75082 Novel human prostasin-like serine protease polypeptide and polymucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.

Claim 1; Fig 1; 111pp; English

This invention comprises the CDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease and reagents and methods for regulating contents of micro-metastasses, autoimmunal fluid. An antibody specific diagnosis of micro-metastasses, autoimmune lesions and renal failure in blopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, ineurodegenerative disease (CPC) approach protein amyloid plaques of Genstmann-Straussler Syndrome, creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease mine the reapeutic target of decreasing human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serine procease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences prostasin-like serine protease #1 nucleotide sequence of the invention which encode the enzyme. The present sequence represents the human

Sequence 537 BP; 92 A; 176 C; 197 G; 72 T; 0 U; 0 Other;

. 0 302 CCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTT Gaps ٥; Score 535.4; DB 6; Length 537; Pred. No. 3e-85; 0; Mismatches 1; Indels 0 . ; 48.6%; Query Match Best Local Similarity 99.8° Matches 536; Conservative

243

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Human; full length cDNA; cDNA synthesis; oligo-capping; Human cDNA 5'-end sequence, SEQ ID NO: 650 AAK92190 standard; cDNA; 670 (first entry) 06-NOV-2001 AAK92190; AAK92190 RESULT

07-JUL-2000; 2000EP-00114089. EP1130094-A2 05-SEP-2001.

Homo sapiens

08-JUL-1999; 99JP-00194486. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765.

(HELI-) HELIX RES INST

Η; Ishii S, Kawai Y; , Otsuki T, Koga s, Hayashi K, K, Kojima kawa T, Isogai T, Sugiyama T, Nagai Nishikawa T, Wakamatsu A, Ota T,

WPI; 2001-524255/58.

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation. SEQ ID NO 650; 1380pp + Sequence Listing; English. Claim 2;

clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA The invention relates to primers for synthesising full length cDNA

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libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nuclectide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-RCM format directly from EPO
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                                                                                                                                                             42.9%; Score 472.8; DB 4; Length 670; 86.9%; Pred. No. 2.9e-74;
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                                                                                                                             Sequence 670 BP; 97 A; 245 C; 205 G; 118 T; 0 U; 5 Other;
                                                                                                                                                                                                81; Indels
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The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence clone which was used in homology searches to identify the clone. Note: The sequence did in homology searches to identify the printed specification, but was obtained in CD-ROM format directly from

Sequence 670 BP; 97 A; 245 C; 205 G; 118 T; 0 U; 5 Other;

830 Primers useful for synthesizing full length cDNA clones and their

in genetic manipulation.

Example 11; SEQ ID NO 1916; 1380pp + Sequence Listing; English.

Η;

Kawai Y; T, Koga

Otsuki Ishii S,

Isogai T, Hayashi K, Is na T, Nagai K, Kojima S,

Nishikawa T, Isog su A, Sugiyama T,

Wakamatsu A,

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WPI; 2001-524255/58

07-JUL-2000; 2000EP-00114089

05-SEP-2001

99JP-00194486

08-JUL-1999;

11-JAN-2000; 2000JP-00118774 02-MAY-2000; 2000JP-00183765

(HELI-) HELIX RES INST

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  Length 670;
                                           Indels
    DB 4;
42.9%; Score 472.8; DB 4; ilarity 86.9%; Pred. No. 2.9e-74; Conservative 0; Mismatches 81;
                   Best Local Similarity
Matches 563; Conserv
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Human; full length cDNA; cDNA synthesis; oligo-capping;

EP1130094-A2 sapiens

Ното

clone representative sequence,

(first entry)

06-NOV-2001 Human cDNA

EXSXEXEXEXEX EXSXEXE

AAK93456;

BP

AAK93456 standard; cDNA; 670

RESULT 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                            Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie;
 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention comprises the cDNA and protein sequences of an isolated
                                                                      CTGGGGAGACNTCCANGGAGGCAAATTCTCTGCCTCTCCCCTGGGTGCTACAAGGAAGTG
TGTCTGCCTGCCCCGCGCGCTCACACGCCTTCGTGCACGGCACCGCCTGCTGGGCCACCGG
                       TGTCTGCCTGCCCCGCGCCTCACACGCTTCGTGCACGGCACCGCCTGCTGGGCACCGG
                                               CTGGGGAGACGTCCA-GGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTAC-AGGAAGTG
                                                                                                                                                                                                                                                                                                                                                                    lipid accumulation;
                                                                                                                                                                                                                                                                                                                                                                                osteoporosis; Paget's disease; ss; EST; expressed sequence tag.
                                                                                                653
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                                                                                                              GAGCTAAGGNIGCTGGGCGAAGGCAACTGGTCAATGICTCTACANNCA
                                                                                              GAGCTAAGGCTGCTGGGCG-AGGCCACCTGTCAATGTCTCTACAGCCA
                                                                                                                                                                                                                                                                                                                                                                  Creutzfeldt-Jakob disease, metastatic cancer;
                                                                                                                                                                                                                                                        Human prostasin-like serine protease cDNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 111pp; English
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                                                                                                                                                                                ABK13566 standard; cDNA; 456
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20-MAR-2001; 2001US-0276909P.
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osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #2 nucleotide sequence of the invention
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0
                                                                                                                                                                                                                                                  Score 442.8; DB 6; Length 456; Pred. No. 5.6e-69; 0; Mismatches 9; Indels 0
                                                                                                                                                                                                             Sequence 456 BP; 74 A; 151 C; 167 G; 62 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #4844.
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                                                                                                                                                                                                                                                                                                447; Conservative
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23-AUG-2000;
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infection. The human prostasin-like serine protesse gene provides a activary, in particular for treating human prostasin-like serine protesse activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat

prostasin-like serine protease and reagents and methods for regulating the human prostasin. Is enzyme activity. Prostasin is a trypsin-like serine protease purified from human seminal fluid. An antibody specific for prostasin-like serine protease is useful for immunodetection and diagnosis of micro-metastases, autoimmune leaions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (Copp), atherosclerosis, neurodegenerative disease (e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, creutzfeldt-Jakob disease, scrapie) or infection, particularly viral

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421 CCAGAGGGCCGCAGGGACACCTGCCAG 447
                                                                                                                                     Matches 445; Conservative
      Drmanac RT, Liu C,
                                                                                                                                 Local Similarity
             WPI; 2001-639362/73
(HYSE-) HYSEQ INC
                P-PSDB; ABG04853
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AAF98698 standard; DNA; 1796 BP AAF98698; RESULT 11 AAF98698 d 셤 ò qq à ₹ The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to traet disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of dara and products dependent on DNA and am to produce other types of dara and products dependent on DNA and am to produce other types of dara and products dependent on DNA and and an activity of and contact defendences and products dependent on DNA and and an activity of and contact defendences and products dependent on DNA and and an activity of a sequences. 300 651 411 531 361 checcederecerrehacerereresenantidechegangerererendenad 420 293 AFGGGACGTTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGC-ACTCCCAGGAC 351 471 coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at GCCTGCTGGGCCACCGGCTGGGAGAAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGG <u> GGGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTAC</u> 121 AGCCAAGTGGAGCTGGGCGCCGACCTGGCCTGCTGCGCCTGGCCTCACCGGCCAGCCTG GGCCCCGCCGTGTGGCCTGTCTGCCTGCCCCGCGCCTCACACGCTTCGTGCACGGCACC GCCTGCTGGGGCCACCGGCTGGGGAACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGG GTGCTACAGGAAGTGGAGCTAAGGCTGGTGGGCGAGGCCACCTGTCAATGTCTCTACAGC CAGCCCGGTCCCTTCAACCTCTCCAGATATTGCCAGGGATGCTGTGTGCTGGCTAC Andedacecnedaececededededenegreerachecreeredesegreerachecae AGCCAAGTGGAGCTGGGCGCCGACCTGGCCTGCTGCGCCTGGCCTCACCGCCAGCCTG GGCCCCGCCGTGTGGCCTGTCTGCCTGCCCCGCGCCTCACACGCTTCGTGCACGGCACC GTGCTACAGGAAGTGGAGCTAAGGCTGCTGGGGCGAGGCCACCTGTCAATGTCTCTACAGC GGGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTAC Gaps New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess 1; 39.3%; Score 433.4; DB 5; Length 597; 99.6%; Pred. No. 2.5e-67; ive 0; Mismatches 1; Indels 1; Sequence 597 BP; 97 A; 217 C; 196 G; 87 T; 0 U; 0 Other; CCAGAGGGCCGCAGGGACACCTGCCAG 738 electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences Claim 1; SEQ ID NO 4844; 103pp; English. Tang YT;

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21-MAR-2000; 2000US-0191321P.
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20-JUL-2000; 2000US-00220467.
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                                                             Human late stage ovarian tumour polynucleotide marker 28
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The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see ARP89834 to ARP98730), in a patient sample; and (2) the normal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated bybridoma, which produces an antibody useful for ovarian cancer assessment, and (3) inhibiting ovarian cancer in a patient. ARF98573 to ARF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene expression profile polynucleotide SEQ ID NO 447.
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Pred. No. 9.2e-32;
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2001US-0301351P.
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Best Local Similarity 54.9
Matches 507; Conservative
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/*tag= a /product= "prostasin-like serine protease" 22-JUN-2001; 2001WO-EP007116. 23-JUN-2000; 2000US-0213474P. 22-MAR-2001; 2001US-0277612P. WO200198466-A2 27-DEC-2001

(FARB) BAYER AG

Xiao Y;

WPI; 2002-114575/15. P-PSDB; ABB07286 Novel human prostasin-like enzyme polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and pathogenic infection

Claim 1; Fig 5; 125pp; English.

The invention relates to human prostasin-like enzyme polypeptides and polymorleotides. The enzyme can be expressed by standard recombinant methodology. The polypeptide, polymorleotide and modulators are useful for treating diseases like metatasis of malignant cells, tunnour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease and pathogenic infection, particularly viral infection. The prostasin-like enzyme gene provides a therapeutic target of decreasing the enzyme activity, in particular for transpenting metastatic cancer. Neurodegenerative diseases include for e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrapie. The agonists and antagonists of the polypeptide may be useful to treat osteoporosis, paget's disease, degradation of bone implants particularly dental implants. Altered levels of human prostasin-like enzyme activity inhibit the progression of restenosis and atherosclerosis. Anti-human prostasin-like serine protease antibodies are useful for immunodetection and inhibit the progression of micrometastases, autoimmune lesions and renal failure in blopsy specimens, plasma samples and body fluids. The protease

Sequence 944 BP; 150 A; 318 C; 318 G; 158 T; 0 U; 0 Other;

213 GAGCCCGCGCGCCGAGTGGTCGCTACTGCTGGGCGTGCACTCCCCAGGACGGGCCCTGGAC 363 124 CCGIACIGCGGGCGCCCIGAGCCCICGGCAICGIGGGGGCTCAAACGCGCAGCCG 183 43 crideccridecidede de constructor GGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCC 243 103 GGAGAGTGGCCGTGGCAGGCAGCATCCAGCATCGTGGGGCACACGTGTGCGGGGGGTCG 162 GCACTGCCAGCTGAGTACCGCGTGCGCCTGGGCTTGCGCTCTGGGCTCCACCTCGCCC 273 GGCGCCCACACCCGCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAG 423 274. cácaciácnich desaga cicandos a casa casa desaga de casa con casa de casa de CTCATCGCCCCCTCCTGGGTCCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTTG 303 crearcacececeanadaraceanaceacecececentecriceceana. 12; Query Match 20.5%; Score 226.4; DB 6; Length 944; Best Local Similarity 57.7%; Pred. No. 5.6e-31; Matches 448; Conservative 0; Mismatches 316; Indels 12 163 184 244 304 à qq à g ð g d ∂ à

δλ	424	CTGGGCGCCGACCTGGCCCTGGCCTGGCCTCACCGCCAGCCTGGGCCCCGCCGTG 483
qq	334	GCCCGCGGCGACCTGCTGCTGCTGCGTCGCCCGGTGCCCCTGAGCGCTCGCGTC 393
Qy	484	TGGCCTGTCTGCCCCGCGCGCCTCACACCGCTTCGTGCACGCAC
ф	394	CAACCCGTCTGCCTGCCCGGCGCCCCGCCCGCCCGCCGGCACACCATGCCGGGTC 453
ζō	544	ACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAA 603
qq	454	ACCGGCTGGGGCAGCCTCCGCCCAGGAGTGCCCCTCCCAGAGTGGCGACGGCTACAAGGA 513
ζŏ	604	GTGGAGCTAAGGCTGCTGGAGGCCACCTGTCAATGTCTCTACAGCCAGC
qq	514	GIAAGGGIGCCGCTGCTGGTCGCGGCGCCTGCTACCACGTGGGCGGGGCGGAC 573
δλ	664	TTCAACCTCACTCTCCAGATATTGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGC 720
qq	574	efeccecagectgagegeattgtgetfectgagagtetgtgtgtgtgecggetacecaggge 633
δλ	721	CGCAGGGACACCTGCCAGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCGC 780
qq	634	CACAAGGAGGCCTGCCAGGGTGATTCTGGGGGACCTCTGACCTGCCTG
Š	781	TGGTTCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAGAAACCGCCCTGGA 840
qa	694	TGGGTCCTGGTGGGGGTGGTGGGGCTGGGGCAGGGTTGTGCCCTGCCCAACCGTCCAGGG 753
λõ	841	GTTTTCACTGCTGCTGCCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTC 896
qq	754	GTCTACACCAGTGTGGCCACATATAGCCCCTGGATTCAGGCTCGCGTCAAGATTAC 809

Search completed: February 25, 2004, 09:18:34 Job time : 482 secs

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FEATURES
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AL190509 QQ49£07.x
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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BB850607 AK078696 BM923713 BB850795	AKU10640 BI763558 BY710051 BB849543 BX436299	BB593614 AZ252377 AK080281 BC034294	BY234907 BY234907 AK006271 BG762809 BM917234	AL578261 CD389322 AK004939 BY235958 CR851297	BY236911 BI259237 BX417595 CA489381 BQ690230 BE590187	CE450243 BY706352 BI554641 BI768651 BX644781 BX644781 CB99595 BY226668 CF900000 CR054579 AK014645	ALIG	lata; ites; nlm,n	Onfulzated (1997) Contact: Robert Strausberg, Ph.D. Bmail: cgapbs-r@mail.nih.gov Oligo-dr track not found, Not I is likely internal to the messag Soares tab Clone distribution: N information can be found through www-bio.llnl.gov/bbrp/image/imagSeq primer: M13 Forward POLYA=NO. Location/Qualifiers
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AI190509 456 bp mRNA linear EST 28-OCT-1998 qd49f07.x1 Soares fetal heart NDHH19W Homo sapiens cDNA clone IMAGE:1732837 3' similar to SW:MCP6_MOUSE P21845 MAST CELL PROTEASE
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LiML; contact the
IMAGE Consortium (infr@mage.llnl.gov) for further information.
Insert Length: 712 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 452.
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ALS51470 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI064YF02 5-PRIME, mRNA sequence.
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(bases 1 to 1071)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12889449.
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/tissue_type="PACENTA" COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
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primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7896.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI064DCO10P1&cluster=7896.r. Contact
Feng Liang Email : fllang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI064DC010P1.
                                                                                                                                                                                                                                                                                                                                                                                                   96 AACTICACTICCAGATATTGCCAGGATGCTGTGTGTGCTGGCTACCCAGAGGGCCGCAGG
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tive 1; Mismatches 374; Indels 16;
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URL:http://genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp/
Carninol.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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and Hayashizaki,Y.
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library (Genome Res. .11 (2), 281-289 (2001)
please visit our web site (http://genome.gsc.riken.go.jp) for
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                          Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matusyama,T., Numasaki,R., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Taqawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 ACTITACGGGTTGGTGCCGTCCGGACCCGCTAGGGGCCCCCCGTACTGCGGGCGCCCTGA
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  Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
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Contact: Yoshihide Hayashizaki
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Location/Qualifiers
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-1771 (2000)
Konno, H., Pukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(62C), Yokohama Institute
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Haytsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 433)
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/clone lib="RIKEN full-length enriched, adult inner ear"
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RIKEN integrated sequence analysis (RISA) system--384-format
                                                 324 GGTACTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGACGGCGCGCACA 373
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Pred. No. 1.9e-25;
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/strain="C57BL/6J"
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Mus musculus
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86.9%;
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Fax: 81-45-503-9216
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Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatau, T., Hiramoto, K., Hiraokar, T., Hirozane, T., Kotim, H., Kayati, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakimura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sagabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, T., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, T.
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-72 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; PROSTASIN (SPTR|BAB82496,
evidence: FASTY, 98.5%ID, 100%length, match=1020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.7%; Score 194.6; DB 1.53.5%; Pred. No. 1.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FANTOM_DB:7530415E19"
/db_xref="MGI:2396949"
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/protein_id="BAC37362.1"
/db_xref="GI:26347427"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/organism="Mus musculus"
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/clone="7530415E19"
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/strain="C57BL/6J"
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length CDRAs
Nature 420, 563-573 (2002)
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                                                                 CCCCGIACTGCGGGGGCCCTGAGCCCTCGGCCATCGTGGGGGGCTCAAACGCGCAGC 181
                                                                                                                                                                                                                                                                                                                           242 CCCTCATCGCCCCCTCCTCGGTCCTCCCCTCTCACTGTTCATGACGAATGGGACGT 301
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
      0; Mismatches
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HTC; CAP trapper.
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SOURCE ORGANISM

AUTHORS TITLE MEDLINE PUBMED REFERENCE AUTHORS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (human) Homo sapiens

ORGANISM

REFERENCE AUTHORS TITLE

EST

1 (bases 1 to 1013) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12804 row: n column: 11
High quality sequence stop: 654.
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                                                                                                                                                                                                                                          /organism="Homo sapiens"

mol type="mRNA"

/db xref="taxon:9606"

/clone="TMAGE:5759434"

/lab_host="DH10B"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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'organism="Mus musculus"
                                                                                                                                                                                           /tissue_type="inner ear"
                                                                                                           /db xref="taxon:10090"
/clone="F930109F10"
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                               /mol_type="mRNA"
/strain="C57BL/6J"
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86.78;
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Best Local Similarity 86.7
Matches 222; Conservative
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Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Grup, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchinco-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashi, X., Shibata, K., Itoh, M., Carninci, P., Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
1 (bases 1 to 433)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB850795
BB850795 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930109F10 5', mRNA sequence.
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   GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAG
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DEFINITION

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 BB850795

ORGANISM

REFERENCE AUTHORS JOURNAL COMMENT

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source

FEATURES

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
/dev_stāgē="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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HPROHACTYTGWGHYAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQ
QDMLCAGYVKGGKMPARVTLGAHSLVPWRASCTWQAL"
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db_xref="GI:26370154"
'translation="MALRVGLGLGQLEAVTILLLLGLLQSGIRADGTEASCGAVIQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="ES cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
Nature 420, 563-573 (2002)
6 (bases 1 to 1629)
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                                        RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                               Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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|db_xref="MGI:1910128"
|db_xref="taxon:10090"
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DB 11; Length 1629;

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Query Match

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BI763558 861 bp mRNA linear EST 25-SEP-2001 603050292F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5190214 5', mRNA sequence..
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           Gaps
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     Mismatches 415; Indels
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DEFINITION
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Mammalia, Bunchia; Rodentla; Schurognath; Murldae; Mullhae; Mushae; 10 (Mazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,T., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Garibodi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gastiooldi,M., Glasi,C., Godzik,A., Gough,J., Grimmond,S., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Lechard,B., Lyons,P.A., Maglott,D.P., Numata,K., Okido,T., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Red,D.U., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneidder,C., Sepule,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Waltanabe,Y., Waltana,R., Yang,I., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hitoxane-Kashikawa,T., Konno,H., Nakanua,M., Yang,I., Rakawa,T., Fukuda,S., Hara,A., Hashizune,W., Imotani,K., Isbii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.
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1010 bp mRNA linear BST 16-DEC-2002
BY710051 RIKEN full-length enriched, ES cells Mus musculus cDNA clone 2410039E18 5', mRNA sequence.

BY710051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTTCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAAAACCGCCCTGGA 840
                                                                           GAGCTGGGCGCCGACCTGGCCCTGCTGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 GAGGACGCCAAGGTCAGCACCCTGAAGGACATCATCCCCCACCCCAGCTACCTCCAGGAG 406
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                             GTGTGGCCTGTCTGCCTGCCCCGCGCCTCACCGCTTCGTGCACGGCACCGCCTGCTGG
                                                                                                                                                                                                                                                     467 Arcedecearcrecerecerecadecaacecerecrrecradedecerecadedecereca
                                                                                                                                                                                                                                                                                                                                                                                 527 GTCACTGGCTGGGGTCATGTGGCCCCCTCAGTGAGCCTCCTGACGCCCAAGCCACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 TCTGGTACTGACGGGGCTTGTGAGCTGGGGACATGCCTGTGGGGCCCGCACAGGCCTGGT
                                                                                                                            407 GGCTCCCAGGGGACATTGCACTCCTCCAACTCAGCAGACCCATCACCTTCTCCCGCTAC
                                                                                                                                                                                                                                                                                                                      GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAG
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Mus musculus (house mouse)
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AUTHORS
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KEYWORDS
SOURCE
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/db xref="taxon:9606"
/db xref="taxon:9606"
/dlone=InARGE:5190214"
/lab host="DHIONE"
/clone=InARGE:5190214"
/lab host="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1:4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAGCCCGCCGCCGAGTGGTCGGTACTGCTGGGGCGTGCACTCCCAGGACGGGCCCCTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GCACCACAAGGAAGCCTATGAGGTCAAGCTGGGGGCCCACCAGCTAGACTCCTACTCC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG 420
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                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 861)
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                                                                                                                                                                                                                              1 (bases 1 to 861)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://mage.llnl.gov
Plate: LLAM11475 row: h column: 23
High quality sequence stop: 861.
Location/Qualifiers
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
BI763558
BI763558.1 GI:15755136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444; Conservative
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                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="KIEN full-length enriched, ES cells"
/clone lib="KIEN full-length enriched, ES cells"
/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primed with a primer [5' GAGAGAGGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                             Email: genome_resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Nondo,S., Konno,H., Koya,S., Miyazaki,A., Nakamura,M., Nakamura,M., Ohno,M., Ohno,M., Ohsato,M., Sato,K., Sato,K., Sato,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation 6 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction of cap-trapper-selected cDNAs to zrepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse fissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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1. .1010
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="2410039E18"
/coll type="RS cells"
/lab_host="SOLR"
                                                                                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                   Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 429)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 AGCAATGACACTGTGGTCCACACAGTGGCTCAGATCATCACCCACTCAAGCTACCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 TACATCAGACCCATCTGCCTCCCTGCAGCCAATGCCTCTTTCCCAACGGCCTTCACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGCCACCGGCTGGGGAGACGTCCAGGAGGAGATCCTCTGCCTCTCCCCTGGGTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCAGCTCGAGGTACCACTCATCAGCCGGGAAACCTGTAGCTGCCTGTACAACATTAAT
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                                                                                                                                            GGCCCCCCGTACTGCGGCCCCTGAGCCCTCGGCCCCGCATCGTGGGGGGCCTCAAACGCC
                                                                                                                                                                                                                      208 GGGACTGAAGCCTCCTGTGGTGCCGTCATCCAGCCACGCATCACCGGTGGTGGCAGTGCA
                                                                                                                                                                                                                                                                                                CAGCCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGG
                                                                                                                                                                                                                                                                                                                                                                      268 AAGCCCGGTCAGTCGCCCTGCCAGCTCACCATCCCTACGATGGCAACCATGTTTGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ACACAGCAGGGAAGCGTATGAGGTGAAGCTGGGGGCCCACCAGCTAGACTCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 CTGGACGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCCAACTACAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGAGCTGGGCGCCGACCTGGCCCTGCCTGGCCCTGGCCTCACCCGCCAGCCTGGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 GAGGGCTCCCAGGGGGACATCGCGCTCATCCGCCTCAGCAGTCCTGTCACCTTCTCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 ACTGTCACGGGATGGGGTCATGTGGCTCCTTCAGTGAGCCTCCAGACCCCTAGGCCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTCGCTCGTGAAATAAATGGGTGTCTGCTGCTGCTGCTTCCCCAGAGA
GIGGCCAAITCIGACICAIACICACIITACGGGIIGGGGCGCCGICCGGACCC
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Mus musculus
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0; Mismatches 387; Indels

Conservative

469;

Similarity

Local Best Loca Matches 검

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Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Inbitrogen. This sequence belongs to sequence cluster 7995.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact :
Feng Liang Bmail: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faradax Avenue Genoscope sequence ID : CSOCAP001AD09FM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mmm." saprems
/mol type="mmm." specific forms
/db xref="taxon:9606"
/dclone="cscorapoolyg17"
/tissue type="mmm." saprems THYMUS"
/clone lib="Homo saprems THYMUS"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligod(T) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB593614 RIKEN full-length enriched, 4 days neonate male adipose Mus musculus cDNA clone B430104M11 5', mRNA sequence.
                                                                                                                                                         930 bp mRNA linear EST 15-WAY-2003
BX436299 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAPOOlYG17
BX436299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGCCGCTGGTTCCAGGCAGGAATCACCAGCTTTGGCTTTTGGCTGTGGACGGAGAAACC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
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Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 171.4; DB 13; 99.4%; Pred. No. 2.1e-20;
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EST.
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         362 ACG 364
                                                            418 AGG 420
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Email: genome-res6gsc.riken.go.jp,
URL:http://genome-res6gsc.riken.go.jp,
Carninof.p., Shibata,Y., Hayateu,M., Sugahara,Y., Shibata,K.,
Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 CCTAGACTGCGGCCGCCCTGAGACCTCTTCCCGCATTGTGGGGGGGCTCGGACGCTCATCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CCCGTACTGCGGGCGCCCTGAGCCCTCGGCCGCATCGTGGGGGGCTCAAACGCGCAGCC 182
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                            RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GGGCACCTGGCCTTGG-CAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCT
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0; Mismatches 37; Indels
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/clone="F930101E02"
/tissue_type="inner_ear"
/dev_stage="adult"
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/strain="C57BL/6J"
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Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Cother GSSs: RPCI-23-466NIS.TJ RPCI-23-466NIS.TVB
Cother GSSs: RPCI-23-466NIS.TJ RPCI-23-466NIS.TVB
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CCAGGAGGCTGTCCCTCTGGCTCTGAGTTCTACAAGAAGTGGAGCTAAGGTTGGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S., Niernan, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pierer de Jong
(pierer@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 466 row: N column: 15
                                                                                                                                                                                                                                                              381 AGTGGCCGCCATCGTGGCGGCCAACTACAGCCAAGTGGAGCTGGGCGGCCGACCTGGC
                                                                                                                                                      2 Adriddicacchrictigaraccidaaaacrachchachdaachddacchdachdach
                                                                                                                                                                                                            122 rdsredcircechactrircecrchiceahcreechecresechecrestressenser
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RPCI-23-466N15.TJB RPCI-23 Mus musculus genomic clone RPCI-23-466N15, genomic survey sequence.
                                                   49; Indels
                         Pred. No. 2.8e-20;
                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="RPCI-23-466N15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:8565580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
                    80.2%;
                 Best Local Similarity 80.2
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ252377
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Fax: 81-45-503-9242

Email: genome-res@gsc.riken.go.jp,

VEL:http://genome.gsc.riken.go.jp,

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,

Sasaki,N., Okazaki,Y., Muramatsu,M. and Haysshizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes

trehalose and its application for the synthesis of full length

CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Okazaki,Y. and Haysshizaki,Y. Shibata,Y., Ozawa,Y., Muramatsu,M.,

Automated filtration-based high-throughput plasmid preparation

Carninci,P. and Haysshizaki,Y.

High-efficiency full-length CDNA cloning. Methods Enzymol. 303,

19-44 (1999)
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 249)

8 Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Murasuyama,T., Miyazaki,A., Nakamara,M., Nishi,K., Nomura,R., Numazaki,R., Okazaki,Y., Shibata,Y., Shamaki,T., Sogabe,Y., Wataniki,A., Yamamura,T., Yasunishi,A., Yoshiki,A., Muranatsu,M. and Hayashiaki,Y. Yoshiki,Y., Yoshiki,Y., RIKEN Mouse ESTS (Aizawa,K. et al. 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3/]. CDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [5' GAGAGAGAGAGAGACATCTTTTTTTTTTTTTTT 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="adipose"
/dev_stage="4 days neonate"
/lab_host="DHIOB"
/clone_lib="RIKEN full-length enriched, 4 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.rtc.riken.go.jp)
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="B430104M11"
     musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               male adipose"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .249
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                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                             REFERENCE
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SOURCE
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GSS 15-JUN-2000

Length 249; DB 10; Score 169.6;

Query Match

/lab host="THIOB"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Corgan: Kidney"/Stain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney_and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size

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selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                 964
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                                                                                                                                                                                                                    100 TCACCAGCITTGGCTTTGGCTGTGGACGGAGGAACGCCCTGGGGTCTTCACTGCAGTGG 159
                                                                                                                                                                                                                                                                                    857 CTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCTGGGCTTGTC 916
                                                                                                                                                         797 reaccaderringedrigingeorgingaacgagaaaaccgcccrggaagrinncacrgcrg
                                                                        Query Match 15.3%; Score 168.6; DB 28; Length 430;
Best Local Similarity 89.4%; Pred. No. 5.1e-20;
Matches 183; Conservative 0; Mismatches 24; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                      220 CCAGCCAGCTCCAGAAGCCACAGTCAG 246
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Search completed: February 25, 2004, 11:17:42 Job time: 2791 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
         Copyright
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February 25, 2004, 08:23:39 ; Search time 112 Seconds (without alignments) 5460.320 Million cell updates/sec

US-10-037-417-45 Perfect score:

Title:

1102 1 999cccttgtcctgggccat......ggggttctgatggggcctcc 1102 Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 682709 segs, 277475446 residues Searched:

1365418

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:* Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1. Appli	ìœ	œ	Sequence 7, Appli	۲,	30.	43	'n	25	25		15, 4	25	m	8	29	H	H	Sequence 18, Appl	1,	18	15.	.0	22	17.	18.	Sequence 13, Appl
SOMMAKIES	US-09-387-375-1	-09-3	US-09-386-642-8	-986-60-	-09-38	US-09-023-942A-30	US-09-620-312D-431	-09-023-	-09-907-794A-2	US-09-905-125A-256	- 1	-09-008-271A-1	US-09-023-942A-25	US-09-023-942A-3	US-09-386-653A-8	-09-386-642	-09-027	US-09-644-600-1	-09-644	-09-624	-09-654	-09-023	US-09-280-116-107	US-09-016-366A-22	-08-97	US-09-016-366A-18	US-08-978-404B-13
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Score	224	ů.	183.2	183.2	165.2	164.2	162	161.6	161.6	161.6	161.6		•	54.	53.	45.			•	٠		140.6	6	139.8	•	φ.	139.8
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Sequence 20, Appl	4,	Seguence 1, Appli Seguence 16, Appl	11, A	Sequence 262, App Sequence 262, App	262,	1, Ap	6	Sequence 9, Appli	6	Sequence 2, Appli	Sequence 28, Appl	10, 4	Sequence 14, Appl	Sequence 20, Appl
US-09-016-366A-20 US-08-978-404B-15	US-09-079-970A-4	US-09-079-970A-1 US-09-016-366A-16	US-08-978-404B-11	US-U9-907-794A-262 US-09-905-125A-262	US-09-902-775A-262	US-09-386-629-1	US-09-027-337-9	US-09-644-600-9	US-09-654-600A-9	US-09-386-629-2	US-09-023-942A-28	US-09-280-116-10	US-09-016-366A-14	US-08-978-404B-20
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1128	771	735	1154	1378	1378	1430	2900	2900	2900	1166	1165	1553	1108	1108
12.5	12.2	12.7	12.1	12.0	12.0	12.0	11.8	11.8	11.8	11.5	11.3	11.2	10.6	10.6
138.2	134.6	133.4	133.4	132.4	132.4	132.4	130.4	130.4	130.4	126.8	124.4	123.6	116.6	116.6
28	30	32	m r	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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129 CTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAGCCGGGCAC 188
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                                                                                                         Sequence 1, Application US/09387375
Patent No. 6485957
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: OI, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT PAPLICATION NUMBER: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 442; Conserv
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RESULT 1
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Gaps

368

379 428 439 488 499

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OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
CTHER INFORMATION: with home sapien serine protease catalytic doma'
US-09-386-642-8
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Pred. No. 1.6e-32;
0; Mismatches 348;
                                                                                                     TCACCCGCCAGCCTGGGCCCCGCCGTGTGGCCTGTCT
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Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Applicade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
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ORGANISM: Artificial Sequence
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Best Local Similarity 53.5%;
Matches 411; Conservative
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EQ ID NO 8
LENGTH: 1142
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US-09-386-642-8
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APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jonson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT AILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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19.7%; Score 216.8; DB 4;
Best Local Similarity 58.0%; Pred. No. 4.1e-40;
Matches 427; Conservative 0; Mismatches 297;
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SEQ ID NO 8
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US-09-387-375-8
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Patent No. 6458564

GENERAL INCRMATION:
APPLICANT: Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Q1, Jian shen
TITLE OF INVENTION: DNA encoding the novel human serine
TITLE OF INVENTION: DNA encoding the novel human serine
TITLE OF INVENTION: DNA encoding the novel human serine
TITLE OF INVENTION: DNA encoding the novel human serine
CURRENT APPLICATION NUMBER: US/09/386,653A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 1
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Pred. No. 1.8e-28;
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ORGANISM: Homo sapiens
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259 CACTGCTTCCCCAGCGA-----GCACCACAAGGAAGCCTATGAGGTCAAGCTGGGG 309
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APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jenson
APPLICANT: Andrade-Gordon, Parricia
TITLE OF INVENTION: Zymogen Activation System
FILE REPRENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT APPLICATION NUMBER: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1169
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Patent No. 6420157
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US-09-386-642-7
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129 CTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAGCCGGGGAC 188
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, FRANK S
REGISTRATION NUMBER: 31,346
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Pred. No. 2.9e-28;
0; Mismatches 328;
                                                                                                                             J3-FEB-1998
                                                         PatentIn Release #1.0,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 436
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ 1D NO: 30:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Best Local Similarity
                                                                                                                                                                                                       FILING DATE: 13
CLASSIFICATION:
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Sequence 30, Application US/09023942A
Fabrat No. 6479274
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                       GACGGGCCCCTGGACGGCGCGCACACCCCGCGAGTGGCCGCCATCGTGGTGCCGGCCAAC
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APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David TITLE OF INVENTION: NOVEL MOLECULES

NUMBER OF SEGUENCES: 30

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY
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GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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14.7%; Score 162; DB 4; Length 1212;
Best Local Similarity 53.6%; Pred. No. 9.4e-28;
Matches 414; Conservative 0; Mismatches 340; Indels 1
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TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: POlypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-04-19
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ. ID NOS: 1105
NUMBER OF SEQ. ID NOS: 1105
SOFTWARE: Pt.-FL_GENES VERSION 1.0
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Patent No. 6569662
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Peiyan
APPLICANT: Chen, Rui-hong
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Wehrman, Tom
Xue, Aidong J.
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US-09-620-312D-431
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ORGANISM: Homo sapiens
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US-09-620-312D-431
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                              841 GITTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTG
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PRIOR APPLICATION NUMBER: PCT/USON/04414
PRIOR APPLICATION NUMBER: PCT/USON/04414
PRIOR PLING DATE: 1099-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: DC/146,222
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-30
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCI/US99/30999
FILING DATE: 1999-12-20
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Timothy A.
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Filvaroff, Ellen
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Roy, Margaret Ann
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wei-Qiang
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Tumas, Daniel
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Pred. No. 1.1e-27;
0; Mismatches 344; Indels
International PCT Application
                                                                                                                                                                                                             REPRENCE DOCKET NUMBER: 1116E
TELECHONE: (516) 742 4343
TELEPHONE: (516) 742 4343
TELEFA: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
TYPE: nucleic acid
STARNDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                               31,346
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52.9%;
                              FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
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Best Local Similarity 52.9<sup>5</sup>
Matches 406; Conservative
                                                                                                                                  NAME: DIGIGLIO, FRA
REGISTRATION NUMBER:
     APPLICATION NUMBER:
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US-09-023-942A-5
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Botstein, David

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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1.1e-27;
0; Mismatches 344;
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2000-02-22
REIGN FILING DATE: 1000-02-22
REIGN FILING DATE: 1999-07-07
REIGN APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-20
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
                                            Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                         Gerritsen, Mary E
                                                                                                                                                              Gerber, Hanspeter
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Matches 406; Conservative
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                      Wei-Qiang
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Tumas, Daniel
                                                                                                              Sherman
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                             Goddard, A.
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Sequence 256, Application US/09905125A Patent No. 6664376 GENERAL INFORMATION:

US-09-905-125A-256

APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi

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Transmembrane Polypeptides and Nucleic
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrant
TITLE OF INVENTION: Secreted and Transmembrant
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/002,775A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-30
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PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-06
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
                                                                                            Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapien
US-09-902-775A-256
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TGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAGCCGGGCACC 189
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Patent No. 6686451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6686451
GENERAL INFORMATION:
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116 recedence de contra de la contra dela contra de la contra del 310 GCGGCCGAGTGGTCGGTACTGCTGGGCGTGC-----ACTCCCAGGACGGGCCCCTG 360 176 TGGCCGTGGCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTC 235 250 GCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTTGGAGCCC 309 236 AGCCACCGCTGGGCACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGAT 295 130 TGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGGCAGCCGGGCACC 190 TGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGGCTCCCTCATC Length 1100; Indels Score 161.6; DB 4; Pred. No. 1.1e-27; 0; Mismatches 344; ; 14.7%; nilarity 52.9%; 1 Conservative 0: Query Match Best Local Similarity Matches 406; Conserv d à qq g à à ð

Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L.

APPLICANT

Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Fong, Sherman, Pong, Wei-Qiang

Ferrara, Napoleone Filvaroff, Ellen

Eaton, Dan L. Desnoyers,

APPLICANT: APPLICANT:

APPLICANT

APPLICANT: APPLICANT:

Ashkenazi, Avi Botstein, David Genentech, Inc.

APPLICANT: GAPPLICANT: APPLICANT:

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249 255 309 360 375 420 435 480 495 555 900 615 099 675 726 780 786 840 846

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52.7%; Pred. No. 2.6e-27;
ive 0; Mismatches 345; Indels
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                                             REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-008-271A-15
                                                                                                                                                                   TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT03
CLONE: 789927
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Matches 405; Conserva
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                                             CCCTCCGGGTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTG
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                                                                                                                                                                                                                 356 cággedracrácácdderracriogrardgaararcrarcrgagdeerogdraddragg
                                                                                                                                                                                                                                                                                                       GAGCTGGGCCCGACCTGGCCCTGCCTGCCTTGGCCTCACCCGCCAGCCTGGGCCCCGCC
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                                                                                                                                   GACGGCGCCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                  GITTICACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTG 888
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN PROTEASE NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto STATE: CA
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US-09-008-271A-15
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199 CIGGACAGICCAGITIGGIGAGCIGACITICCAGGCCAICTCTCTGGAACCIACAGGCCIA 258
                                                                               369 GCACACCCGCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGG 428
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                                                                                                                                                                                                                                                                                                           319 CAATGACATAGCCCTGCTGAAGCTGTCATCTCCAGTCACCTACAATAACTTCATCCAGCC
                                                                                                                                                       259 TTCCAACCGTTACCAAATAGAAGATATTTTCCTGAGCCCCCAAGTACTCGGAGCAGTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           549 CTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAAGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 TGCCTGCTTTGGTGACTCGGGAGGACCCTTGGCCTGCGACCAGGATACGGTGTGGTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          789 GGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAGAAACCGCCCTGGAGTTTTCAC
                                                                                                                                                                                                                               429 CGCCGACCTGGCCCTGCTGCCCTCACCCGCCAGCCTGGGCCCCGCCGTGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                   489 TGTCTGCCCCGCGCGCTCACACCCTTTCGTGCACGCCACCGCCTGCTGCTGCGCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David TITLE OF INVENTION: NOVEL MOLECULES NUMBER OF SEQUENCES: 30 NORRESPONDENCE ADDRESSS: ADDRESSSE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                International PCT Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY PLAZA CITY: GARDEN CITY PLAZA CITY: GARDEN CITY STATE: NEW YORK COUNTRY: USA COUNTRY: USA COUNTRY: USA CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBN: PC-DOS/MS-DOS COUNTRY DE COMPATIBN: PC-DOS/MS-DOS COUNTRY DE COMPATIBN: PC-DOS/MS-DOS
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CLASSIFICATION: 435
IOR APPLIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09023942A Patent No. 6479274 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATE:
FILING DATE: 18-NOV-1997
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCCCTCAT 248
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                                                                                                                                       Sequence 25, Application US/09023942A

Patent No. 6479274

GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ALDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,942A

FILING DATE: A3-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PO5101/97

FILING DATE: 13-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P0422/97

FILING DATE: 18-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: International PCT Application FILING DATE: 13-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: D137GLIO, FRANK S

REGISTRATION NUMBER: 31,346

PRIOR PROPERTION NUMBER: 31,346

PRIOR PROPERTION NUMBER: 31,346
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Pred. No. 8.8e-27;
0; Mismatches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.3%;
ilarity 52.4%;
Conservative
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nucleic acid
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MEDIUM TYPE: Floppy
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ses 377; Conserv
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 154.8; DB 4; 52.2%; Pred. No. 3.9e-26; iive 0; Mismatches 352;
TELEPANE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            LENGTH: 1094 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 52.2
Matches 398; Conservative
                                                                                                                                                                                                                                                                                                                 CDS
17..955
                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: Protease T in a zymogen activation vector
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14.0%; Score 153.8; DB 4; Length 1
Best Local Similarity 53.9%; Pred. No. 6.6e-26;
Matches 392; Conservative 0; Mismatches 317; Indels
                                                                                                                                                                                                                                 APPLICANT: Darrow, Andrew APPLICANT: Qi, Jian-shen TITLE OF INVENTION: DNA encoding the novel human serine TITLE OF INVENTION: Drotease T FILE REFRENCE: ORT-1032 CURRENT FILION NUMBER: US/09/386,653A CURRENT FILION DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 8 LENGTH: 1130
Sequence 8, Application US/09386653A Patent No. 6458564
                                                                                                                          GENERAL INFORMATION:
APPLICANT: Andrade-Gordon, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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871 TGGATAC 877 ||||||| 874 TGGATCC 880

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Search completed: February 25, 2004, 11:19:47 Job time : 118 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 52, Appl	Sequence 447, App	_	Sequence 25, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Seguence 2214, Ap	Sequence 141, App	Sequence 261, App	Sequence 208, App	~	Sequence 8, Appli	Sequence 8, Appli
	ID	US-09-888-615-52	US-10-101-510-447	US-10-176-847-85	US-10-051-874-25	US-10-041-400A-1	US-10-041-264A-1	US-10-042-091A-1	US-09-948-094-1	US-09-880-107-2214	US-09-967-768A-141		US-09-925-301-208	US-10-041-400A-8	US-10-041-264A-8	US-10-042-091A-8
	DB	9	14	14	15	13	13	13	σ	σ	6	14	6	13	13	13
	Query Match Length DB	2457	3382	1733	1020	1613	1613	1613	1834	1834	1834	1834	1668	1130	1130	1130
ф	Query	74.0	21.1	20.9	20.5	20.3	20.3	20.3	20.1	20.1	20.1	20.1	20.0	19.7	19.7	19.7
	Score	815.6	232.4	230.8	225.6	224	224	224	221.2	221.2	221.2	221.2	220.6	216.8	216.8	216.8
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ALIGNMENTS

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184 GGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCCACATCTGCGGGGGCTCC 243
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                                                                                                                                                                                                                             APPLICANT: PLOWARM, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CHANFDELL, SEAN
APPLICANT: CHANFDCZAK, GLEN
APPLICANT: CHANFDCZAK, GLEN
APPLICANT: CHANTOCAK, GLEN
APPLICANT: WIDARSANM, SUCHA
APPLICANT: WIDARSANM, SUCHA
APPLICANT: SUDARSANM, SUCHA
TILLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 52
SEQ ID NO 52
                                       Sequence 52, Application US/09888615; Patent No. US20020064856A1; GENERAL INFORMATION:
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Best Local Similarity 99.5
Matches 818; Conservative
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; ORGANISM: Homo sapiens
US-09-888-615-52
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US-09-888-615-52
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APPLICANT: Veiby, Petter Ole
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
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US-10-176-847-85
Sequence 85, Application US/10176847
Publication No. US20030068636A1
GENERAL INFORMATION:
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Pred. No. 2.4e-51;
0; Mismatches 401; Indels
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Publication No. US20030148295A1

GENERAL INFORMATION:

APPLICANT: WAN, JACKSON

TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF 17

FILE REFERENCE: 15117.0012

CURRENT APPLICATION NUMBER: US/10/101,510

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: 60/276,947

PRIOR APPLICATION NUMBER: 60/276,947

PRIOR APPLICATION NUMBER: 2001-03-20

NUMBER OF SEQ ID NOS: 805

SOFTWARE: PATENTIN VOE: 2.1

SEQ ID NO 447
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Best Local Similarity 55.0
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APPLICANT: BURGES, Catherine E
TITLE OF INVENTION: PROTEINS, POLYNUCLECTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: BING THE SAME
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FILLE OF TOWERT POLYCE DATE: 2002-09-25
GURRENT FILLING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR PILLING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR FILLING DATE: 2001-09-27
PRIOR FILLING DATE: 2001-02-28
PRIOR FILLING DATE: 2001-01-18
PRIOR FILLING DATE: 2001-01-18
PRIOR FILLING DATE: 2001-01-18
PRIOR PELLOR NUMBER: 60/262,454
PRIOR PELLOR NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR PILLING DATE: 2001-01-16
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906 GIGIACACTICTGGCTTCCAGCTATGCCTCGGATCCAAAGCAAGGTGACAAACTCCAG 965
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APPLICATION VUNBER: 60/330,336
FILING DATE: 2001-10-18
APPLICATION NUMBER: 60/265,530
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APPLICATION NUMBER: 60/261,376
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No. US20040005557A1
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Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
Liu, Xiaohong
Ellerman, Karen
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APPLICANT: Alsobrook II, John P
PAPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
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Herrman, John L
Peyman, John A
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Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
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Edinger, Shlomit R
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Tchernev, Velizar
Zerhusen, Bryan D
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Smithson, Glennda
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Shenoy, Suresh G
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Stone, David J
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Pred. No. 5.9e-51;
0; Mismatches 402;
      TITLE OF INVENTION: AND OVARIAN CANCER
FILE REFREENCE: MRI-039
CURRENT APPLICATION NUMBER: US/10/176,847
CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFFWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 85
LENGTH: 1733
                                                                                                                                                                                                                                                                                                                                                                             20.9%;
54.9%;
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Matches 507; Conservative
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 1.3e-49;
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PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 1020
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Best Local Similarity 58.0°
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Sequence 1, Application US/10041400A Publication No. US20020110895A1 GENERAL INFORMATION:
APPLICANT: Darrow, Andrew APPLICANT: Andrade-Gordon, Patricia

RESULT 5 US-10-041-400A-1

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APPLICANT: Qi, Jenson
TITLE OF INVENTION: DATA Encoding the Human Sering OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
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APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: A., Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
                                                                                                          Sequence 1, Application US/10041264A Publication No. US20020142446A1 GENERAL INFORMATION:
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No. 3.6e-49; Conservative 0; Mismatches 310; Indels
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Sequence 1, Application US/10042091A

Publication No. US20020142447A1

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
TITLE OF INVENTION: DAR Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031

CURRENT APPLICATION NUMBER: US/10/042,091A

CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375

PRIOR APPLICATION NUMBER: US/09/387,375

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1
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481 GTGTGGCCTGTGCCTGCCCGCGCTTCACACCGCTTCGTGCACGGCACCGCCTGCTGG
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Patent No. US20020142981A1
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Best Local Similarity 54.2<sup>3</sup>
Matches 501, Conservative
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Patent No. US20020090625A1
GENERAL INFORMATION:
APPLICANT THE BYIGHAM and Women's Hospital, Inc.
APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
FILE RFERENCE: 81994/282423
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT APPLICATION NUMBER: US/09/948,094
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tive 0; Mismatches 408;
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SOFTWARE: PatentIn version 3.0
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GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950
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US-09-880-107-2214
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Patent No. US20020150877A1
GRERAL INFORMATION:
GREIGANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Set
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/69/967,76BA
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR PELING DATE: 2000-09-28
PRIOR PELING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
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445 TCTCTCGTGTCTGAGCAGTGCTGTCAGCTGCTGCTCCCCAGCGA---
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
CURRENT FILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER: OF SQL ID NOS: 1694
SOFTWARE: PATCHTIN UVER: 2.0
SEQ ID NO 208
LINGTH: 1668
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Patent No. US20020052308A1
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LOCATION: (1505)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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US-09-925-301-208
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REPREENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT PILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/225,149
PRIOR APPLICATION NUMBER: 60/225,149
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                        RESULT 1.

10S-10-097-340-261

1 Sequence 261, Application US/10097340

2 Publication No. US20030087250A1

2 GENERAL INFORMATION:

APPLICANT: Ohn MONAHAN

APPLICANT: Shubangi KAMATKAR

APPLICANT: Shubangi KAMATKAR

APPLICANT: Steve G. KOVATS

APPLICANT: Rachel E. MEYERS

APPLICANT: Rachel E. MEYERS

APPLICANT: Rachel E. MEYERS

APPLICANT: Peter OLANDT
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Robert C. BAST, Jr.
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Best Local Similarity 54.2
Matches 501; Conservative
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ORGANISM: Homo sapiens
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CTHER INFORMATION: Description of Artificial Sequence: Nucleic acid;

OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application US/10041400A; Publication No. US2020110895A1
; Beublication No. US2020110895A1
; GENERAL INFORMATION;
; APPLICANT: Dairrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/10/041,400A
; CURRENT APPLICATION NUMBER: US/09/387,375
; PRIOR PLING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 8
; SEQ ID NO 8
                                                                                                                                                                                                                                           GCCTCGTGTGCTCCCAAACCCAAG 1100
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2; Mismatches 401;
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                                                       CTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature 1.0CATION: (1598)
CTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature 1.0CATION: (1620)
CTHER INFORMATION: n equals a,t,g, or US-09-925-301-208
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Best Local Similarity 54.7%;
Matches 506; Conservative
LOCATION: (1565)
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                                                                        577 creccagagegegaccaccactacaagaagiaaagargeccacracragacregogacrego
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                                                                                                                                                                                                                                                                                                               GGCTGTGGACGGAGAAACCGCCCTGGAGTTTTCACTGCTGTGGCTACCTATGAGGCATGG
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58.0%; Pred. No. 2.7e-47;
tive 0; Mismatches 297; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrede-Gordon, Patricia
APPLICANT: Qi, Jenson
ITLLE OF INVENTION: DNA Encoding the
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10042091A Publication No. US20020142447A1
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US-10-042-091A-8
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Publication No. US20020142446A1
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Oi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
TITLE REPERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,264A
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Artificial Sequence
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February 25, 2004, 11:19:55; Search time 4327 Seconds (without alignments) 11038.600 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX512287 Sequence AX512289 Sequence	AX360096 Sequence	AX480935 Sequence BD127529 Primer fo	AK075142 Homo sapi	AX342934 Sequence AX342936 Sequence	BD125219 Primer fo	AC009088 Homo sapi	AC135044 Homo sapi	AC093520 HOMO Sapi AX098193 Sequence	BC001462 Homo sapi	AX098215 Sequence U33446 Human prost	AC135044 Homo sapi	AX335777 Sequence	AX336076 Sequence	AX409567 Sequence	Seg	AX193364 Sequence	BC035589 Homo sapi	AB002294 Human mRN AC135050 Homo sani	Segue	AC124816 Mus muscu	ACIOI465 Mus muscu	ACC093175 Mus muscu	AC106629 Rattus no	ACII/I/O KACCUS IIO AXS12409 Seguence	AX556574 Sequence	AC020159 Drosophil	393	AE003698 Drosophil	AX369313 Sequence AR263844 Sequence	54 Dog			linear PAT 27-SEP-2002				Vertebrata; Euteleostomi; ; Hominidae; Homo.	, Liu,X., Spytek,K.A., Burgess,C.E., Vernet,C.A., Ellerman,K., Malyankar,U.,
SUMMARIES B ID	6 AX512287 6 AX512289																					AC101465	0 0									ALIGNMENTS		1102 bp	atent WO02 92631	9	c	Chordata; Craniata; Primates; Catarrhini	.P., Tchernev,V.T. W.M., Lepley,D.M., ger,S., Sciore,P.,
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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U., Rothenberg,M., Stone,D., Shenoy,S. shenoy,S. and Anderson,D. Proteins and nucleic acids encoding same
Patent: WO 02053742-A. 45 11-JUL-2002;
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           GTTTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAG 900
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1102; Conservative 0; Mismatches
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                       Manning, G., Caenepeel, S.
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Plowman, G., Whyte, D., Sudarsanam, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: WO 0200860-A 52 03-JAN-2002;
Sugen, Inc. (US)
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Homo sapiens (human)
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TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2010)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITCATGACGAATGGGACGITGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2960 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0245383-A 31 13-JUN-2002;
Incyte Genomics, Inc. (US)
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/organism="Homo sapiens"

/ Organia - Mana	Query Match 57.3%; Score 631; DB 9; Length 2810; Best Local Similarity 99.6%; Pred. No. 0; Matches 781; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 162 GGGGGGCTCAAACGCGCAGCCGGGCACCTGGCCTTGGCACCACCATGGAGG 221 11	Qy 222 TRACCACATCTGCGGGGGCTCCTCCTCCTCCTCCTCCTCGTGGTC
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Frimer for synthesizing full-length cDNA linear PAT 18-SEP-2002 BD125219 BD125219 GI:23220164 GI:2322017375-A/650.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of human prostasin-like serine protease
Patent: WO 0198467-A 3 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          linear
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                          Sequence 3 from Patent W00198467.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation of human prostasin-like serine protease
Patent: WO 0199467-A 1 27-DBC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 670)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 GGGGGGCTCAAACGCGCAGCCGGGCACTTGGCCTTTGCAAAGTGAGCCTGCACCATGGAGG
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                                                                                                                                                                                                                                                      Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 1916 22-JAN-2002; HELIX RESEARCH INSTITUTE
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Location/Qualifiers
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99.7%; Pred. No. 6.3e-171;
tive 0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002017375-A/1916
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SHINICHI KOJIMA,
        Homo sapiens
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                                                                                                                                                                                            Primer for synthesizing full-length cDNA and use thereof Patent: JP 202017375-A 650 22-JAN-2002; Patent: JP 202017375-A 650 22-JAN-2002; HELIX RESEARCH INSTITUTE
OS HOMO sapiens (human)
PN JP 2002017375-A/650
PP 72-JAN-2002
PP 77-JUL-2000 JP 2000253172
PP TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAXASHI, SHIZUKO
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 670)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
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Primer for synthesizing full-length cDNA and use thereof. BD126485
BD126485.
GI:23221430
JP 2002017375-A/1916.
Homo sapiens (human)
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HTG 05-OCT-2002
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Submitted (05-OCT-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 195476)
DOE Joint Genome Institute.
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Consensus quality: 182638 bases at least Q30
Consensus quality: 188055 bases at least Q30
Consensus quality: 188055 bases at least Q30
Estimated insert size: 170000; agarcse-fp estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agarcse-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* Consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                       AC135044 195476 bp DNA linear HTG 05-C
HOMO sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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-----Genome Center
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Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
National Laboratory
Www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 80.2.
NOTE: This insert is not the entire sequence of the clone (entire Sequence is 233.4kb). It is clipped at the overlap with AC135050.
The number of bases overlapped is 2575.
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                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-APR-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 127769)
                                                                                                                                                                                                                                                   Submitted (03-AUG-1999) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 127769)

DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 Chases I to 127769) USA DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Submitted (29-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 0D Drive, Walnut Creek, CA 94598, USA ON MAR 29, 2003 this sequence version replaced gi:29029216.

Draft Sequence Produced by DOE Joint Genome Institute
                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 127769)
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Direct Submission
                                                                                                                     DOE Joint Genome Institute, Stanford Human Genome Center and Los
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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DOE Joint Genome Institute.
Direct Submission
                                                                                                                                       Alamos National Laboratory.
Direct Submission
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Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laborator:
National Laboratord.edu
Quality: Phrap Quality >= 40 100% of Sequence;
Estimated Total Number of Errors is 0.
Location/Qualifiers
                                                                3 (Dases 1 to 16864)
DoE Joint Genome Institute.
Direct Submission
Submitted (13-JUN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (Dases 1 to 168064)
Direct Submission
Submitted (07-JUL-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA USA USA (Dases Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
                        DOE Joint
94598, USA
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-MAR-2003) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 19, 2003 this sequence version replaced gi:21702833. Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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Direct Submission
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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100.0%; Pred. No. 2.5e-34;
ive 0; Mismatches 0;
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
Direct Submission
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Homo sapiens chromosome 16 clone RP11-120K18, complete sequence.
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// Organism="Homo sapiens"
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// Chromosome="16"
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// Clone="CalTech human BAC library D"
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Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse oDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                      BC001462 1800 bp mRNA linear PRI 04-OCT-2003 Homo sapiens protease, serine, 8 (prostasin), mRNA (cDNA clone MGC:2133 IMAGE:3138532), complete cds.
                                                          ö
                                                                                                                                                               134 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGGCCTGGGGCAGCTGGGGGCT
                                                          Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (18C),
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
on Aug 19, 2003 this sequence version replaced gi:12655206.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                          .,
  Length 1796;
                                                        0; Indels
                             1.3e-23;
     DB 6;
                          100.0%; Pred. No. 1.3 ive 0; Mismatches
     Score 67;
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                       Similarity 100.
67; Conservative
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Query Match
Best Local &
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JOURNAL
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BC001462
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                                                        Matches
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KEYWORDS
SOURCE
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COMMENT
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HQLDSYSEDAKVSTIKOTTPHPSYLQEGSQGDTALLQLSRPTTFSRYTRPICLPAANA
SFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQ
EDMYCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASS
                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAL Plate: 4 Row: j Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536453.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="LocusID:5652"
/translation="WAQKGVIGPGQLGAVAILLYLGLLRSGTGAEGAEAPCGVAPQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YASWIQSKVTELQPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG
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McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITGGSSAVAGOWPWOVSITYEGVHVCGGSLVSEOWVLSAAHCFPSEHHKEAYEVKLGA
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/note="Tryp_SPc; Region: Trypsin-like serine protease"
/db_xref="CDD:smart00020"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Placenta, choriocarcinoma"
/clone_llb="NIH MGC 21"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="prostasin preproprotein"
/protein_id="AAH01462.1"
/db_xref="G1:12655207"
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100.0%; Pred. No. 1.3e-23;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:2133 IMAGE:3138532"
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/db_xref="LocusID:5652"
/db_xref="wIM:600823"
176_.1207
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/organism="Homo sapiens"
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ABQ93901 standard; DNA; 1102 BP
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9855.820 Million cell updates/sec
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                                                                                              February 25, 2004, 11:17:50 ; Search time 475 Seconds
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Abq75956
Aak94500
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                    3373863 segs, 2124099041 residues
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ABQ93902
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geneseqn2001as:*
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Aai29377 Colon tum	Abz33563 Human col	Aba21236 Human ner	Abn85393 Human NOV	Aac77814 Human can	Aas26531 Human cDN	Human	Aas26109 Human cDN	Abx73450 Human nov	Abk13570 Prostasin	Abq93931 Human NOV	Abs52114 Human bet	Н		Abl18082 Drosophil	Aad27724 Human tra	Abk30252 Human G-p	Abg83347 Human KLK	Aaa95896 Human KLK	Abk31801 DNA encod	Human	Abk30258 Human G-p
AA129377	ABZ33563	ABA21236	ABN85393	AAC77814	AAS26531	ABX73872	AAS26109	ABX73450	ABK13570	ABQ93931	ABS52114	ABL29631	ABL29630	ABL18082	AAD27724	ABK30252	AB083347	AAA95896	ABK31801	ABK30259	ABK30258
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ALIGNMENTS

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Human; NOVX; neurological disorder; Alzheimer's disease;

W Humtington's disease; Parkinson's disease; pain; behavioural disorder;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;

KW thyroiditis; ardiovascular disease; hypertension; reproductive disorder;

KW thyroiditis; incontinence; psoriasis; scleroderms; alopecia;

KW pancreatitis; cirrhosis; glomerular endocheliosis; bacterial infection;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

M atherosclerosis; cell signal processing-related disorder;

KW antiinflammatory; immunosuppressive, analgesic; antiatherosclerotic;

KW dermatological; antibacterial; antiarthritic; hepatotropic; neuroprotective;

KW defferentiation; proliferation; motility; haematopoiesis; wound healing;

KW gene therapy; NOV14a; prostatin precursor-like; chromosome 16; gene; ds.
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                                                               Human prostatin precursor-like NOV14a DNA, SEQ ID NO:43.
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08-JAN-2001; 2001US-0260360P-
28-FEB-2001; 2001US-0272411P-
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CCCCCGTACTGCGGGCGCCCTGAGCCCTCGGCGCCATCGTGGGGGGCCTCAAACGCGCAG

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05-JUL-2001, 2001US-0303231P.
12-JUL-2001, 2001US-0305660P.
10-SEP-2001, 2001US-0318405P.
12-SEP-2001, 2001US-0318700P.
04-JAN-2002, 2002US-00037417.
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02-MAR-2001;
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ï Ë ä Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA; Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U; Rothemberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson I Padigaru M, Taupier RJ, Miller CE, Eisen A;

WPI; 2002-583619/62. P-PSDB; ABB09523.

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders

Claim 9a; Page 142; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleotides are useful in the treatment, diagnosis or prevention of NOVX-associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24 NOVX proteins, based on their homology to known proteins. Various cisorders (e.g., Albreimer's, Huntington's and Parkinson's diseases), disorders are associated with NoVX proteins including neurological disorders (e.g., Albreimer's, diabetes, thyroiditis, candiovascular disorders, or an autoinmune diseases), pain, behavioural disorders, diabetes, thyroiditis, cardiovascular disorders (e.g., Albreimer's), diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, asthma, various formsorlar endotheliosis, polycystic kidney disease, endocrine (e.g., hypertension), reproductive disorders, panoreatitis, circhosis, glomerular endotheliosis, polycystic kidney disease, endocrine (e.g., hypertension), reproductive disorders and disorders atherosclerosis, cell signal processing-related disorders and disorders atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regularion. NoVX nucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which as neurogenesss, cell differentiation, cell motilise or inhibit processes such as neurogenesss, cell differentiation, cell motilise or inhibit and conting NOVX nucleic acids are used to identify a cell of determination of small models are used to identify and cloning NOVX nucleic acids are useful as course of primers or probes for forear or nucleic acids and forear information and ransagenic animals which are useful for studying the function and transgenic animals which of NOVX activity. The present sequence represents DNA encoding the prostatin precursor-like protein NOV14a. The gene encoding NOV14a is located on chromosome 16

Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other;

DB 6; Length 1102;

9 GGGCCCTTGTCCTGGGCCATGGCCCAGGAGGGGGTCCTGGGGCCTGGGGCAGCTGGGGGCCT GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCT 0; Gaps 0; Indels 100.0%; Score 1102; 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 1102; Conservative à g

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01-NOV-2002 AB093902;

(first entry)

panceatitis, incontinence, psoriasis, scleroderma, alopecia; ulcer; panceatitis, cirrhosis, glomerular endotheliosis, bacterial infection; polycystic kidney disease, endocrine disorder; obesity, cardiomyopathy; atherosclerosis, cell signal processing-related disorder; cardiomyopathy; antibothway regulation disorder; cytostatic; neuroprotective; antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic; dermatological; antibacterial; antiatrhitic; hepatotropic; neurogenesis; differentiation; proliferation; motility; haematopoiesis; wound healing; angiogenesis; forensic biology; transgenic animal; drug screening; gene therapy; NOVL4b; prostatin precursor-like; gene; ds. thyroiditis; cardiovascular disease; hypertension; reproductive disorder; Huntington's disease; Parkinson's disease; pain; behavioural disorder; addiction; tuberous sclerosis; cancer; immune disorder; allergy; autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes; Human; NOVX; neurological disorder; Alzheimer's disease; Human prostatin precursor-like NOV14b DNA, SEQ ID NO:45. Location/Qualifiers /product= "NOV14b" 1093. .1102 /*tag= c 05-JAN-2001; 2001US-0260018P. 08-JAN-2001; 2001US-0250350P. 02-MAR-2001; 2001US-0272411P. 05-JUL-2001; 2001US-037321P. 12-JUL-2001; 2001US-0305050P. 10-SEP-2001; 2001US-0318405P. 12-SEP-2001; 2001US-0318700P. 07-JAN-2002; 2002WO-US000375 2002US-00037417 ๙ /*tag= b 19. .1092 /*tag= WO200253742-A2 12-SEP-2001; sapiens 11-JUL-2002 Key 5'UTR 3'UTR Ношо CDS

(CURA-) CURAGEN CORP

Spytek KA; CE, Vernet CAM, Tchernev VT, Liu X, Spyce.
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2002-583619/62.

P-PSDB; ABB09524

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune Claim 9a; Page 143; 323pp; English. disorders

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The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX-associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24

NOVX proteins, based on their homology to known proteins. Various disorders are associated with NOVX proteins including neurological calcasorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tuberous sclerosis, cancers (e.g., colorectal cancer, leukaemia and osteosarcoma), immune diseases (e.g., allergies and autoimmune diseases), mysathenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, asthma, corringes, psoriasis, scleroderma, alopecia, ulcers, pancreatiis, cirhosis, glomerular endotheliosis, polycystic kidney disease, endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. Novx nucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which binds to a NoVx protein, and are also useful as targets for the constitutioation of small molecules that modulate or inhibit processes such identification of small molecules that modulate or inhibit processes such as neurogenesis, cell differentiation, cell motility, cellular corrected as sequences can be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic biology and for identifying and cloning NoVx homologues in other cell types. Cells comprising NOVX nucleic acids are useful for studying the function and cranimals which are useful for studying the function and confine and persent sequence represents DNA encoding the 9 1 gescerrierenceseceareseceasaasesesrerreseseerresecaserreseseer 1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGCCT Gaps ٠, 6; Length 1102; Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other; Indels 0, DB 100.0%; Score 1102; 100.0%; Pred. No. 0; 0; Mismatches prostatin precursor-like protein NOV14b Best_Local Similarity 100. Matches 1102; Conservative Query Match 8\$ à

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Nucleic acids encoding novel human proteases, useful for useful

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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and disorders (e.g. inflammatory thrombosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. restenosis en continuous pain, sexual dysfunction, mood disorders, attention disorders, hypotension, hypertension, psychotic disorders, cognition disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (b.g. virus (HIV)).
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Lal PG, Walia NK, Hafalia AJA, Gandhi AR, Au-Young J, Elliott VS;
Ramkumar J, Thangavelu K, Iu Y, Warren BA, Iu DAM, Lee EA;
Tribouley CM, Arvizu C, Delegeane AM, Yao MG, Khan FA;
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19-JAN-2001; 2001US-0262851P.
25-JAN-2001; 2001US-0264623P.
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P-PSDB; ABB98135.
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Sanjanwala MM;
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New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.

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The invention relates to an isolated Protein Modification and Maintenance (PMM) polypeptide. Polypeptides of the invention may be used in the diagnosts, treatment and prevention of disorders associated with accreased expression or activity of PMMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. en) typertension), autoimmune/inflammatory disorders (e.g. anaemia), cell hypertension), neurological disorders (e.g. Alzheimer's disease) creproductive disorders (e.g. Alzheimer's disease) creproductive disorders (e.g. ectopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the cffects of exogenous compound on the expression of nucleic acid and amino acid sequence represents a human PMMMM encoding sequence of the invention, encoding a polypeptide which has been found to have homology
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Pred. No. 0
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Best Local Similarity 99.8
Matches 816; Conservative
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                                                                                                                                                                                                                                                                                                                                  full length cDNA; cDNA synthesis; oligo-capping; ss.
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99.6%; Pred. No. 1.9e-284;
ive 0; Mismatches 3; Indels
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Sugiyama T, Nagai K, Kojima S, Otsuki
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                                                                                         CTGCCTTTCCCACCCAGCCCCAGAAGACCCCAGTCAGAT
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02-MAY-2000; 2000JP-00183765.
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TITCATGACGAATGGGACGTTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCA 341

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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide, osteopathic; antinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tunour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease, COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; awyloid plaque; Genstmann.Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss.
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complement(3...536)
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/note= "No start or stop codons shown"

'product= "Prostasin-like enzyme"

partial

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23-JUN-2000; 2000US-0213588P.
20-MAR-2001; 2001US-0276909P.
                     22-JUN-2001; 2001WO-EP007117
                                                2002-114576/15
                                          Xiao Y, Morozov V;
                                    (FARB ) BAYER AG
                                                   P-PSDB; AAU75082
           WO200198467-A2
                 27-DEC-2001
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This invention comprises the cDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like care protease is useful fluid. An antibody specific the human protease purified from human seminal fluid. An antibody specific for prostasin-like serine protease is useful for immunodetection and diagnosis of micro-metastases, autoimmune lesions and renal failure in complete enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive used to modulate enzyme activity in a disease, such as metastasis of collmonary disease (CDD), atherosclerosis, neurodegenerative disease (CDD), atherosclerosis, neurodegenerative disease (CDD), atherosclerosis, neurodegenerative disease (CDD), atherosclerosis, neurodegenerative disease (CDT), atherosclerosis, neurodegenerative disease (CDT), atherosclerosis, neurodegenerative disease crivity, in particular for treating or infection, particularly viral infection, particularly dental implants. Altered levels of human prostasin-like serine protease activity which may be useful to treat operaticularly dental implants. Altered levels of human prostasin-like corpusions and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic and lipid accumulation and inhibit the sormal sequence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #1 nucleotide sequence of the invention ö Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections. Gaps ., Length 537; 1; Indels Sequence 537 BP; 92 A; 176 C; 197 G; 72 T; 0 U; 0 Other; Claim 1; Fig 1; 111pp; English

482 422 302 478 362 418 358 cercardececetecreserecretecersererrarearsarsarsars GGAGCCCGCGGCCGAGTGGTCGGTGCTGGCGTGCACTCCCAGGACGGCCCCTGGA CGGCGCGCACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGA gerragaciacios y consecución de conse CCTCATCGCCCCCTCCTGGGTCCTCCCGCTGCTCACTGTTCATGAAATGGGACGTT 477 genecececedes de producto de la constanta del constanta de la constanta de 44.1%; Score 486; DB 6; I 99.8%; Pred. No. 1.1e-216; iive 0; Mismatches 1; Conservative Local Similarity tes 536; Conserv 243 537 303 363 423 Query Match Matches

ð a ò g à q

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treat disease tates involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease tates involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The CTICAACCICACICICCAGAIAIIGCCAGGGAIGCIGIGIGCIGGCIACCCAGAGGGCCG 722 602 662 cricaaccrcacrcrcadarafreccaddargrererereregecradcadagadde 58 CAGGGACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCG 779 357 GCIGGGCCCGACCIGGCCCIGCCGCCTCGCCTCACCCGCCAGCCIGGGCCCCGCCGT GTGGCCTGTCTGCCCCCCCCCCCCCCCCCTCGCTGCACGGCACCGCCTGCTGGGC CACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGA cadegacaccideccadaginaaciiciidaddagceeeeridaiciidigaadaadagacce 1 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess DNA encoding novel human diagnostic protein #4844. claim 1; SEQ ID NO 4844; 103pp; English. ВР Tang YT; 30-MAR-2001; 2001WO-US008631. 2000US-00540217 2000US-00649167 AAS69040 standard; cDNA; 597 (first entry) Liu C, WPI; 2001-639362/73 (HYSE-) HYSEQ INC P-PSDB; ABG04853. WO200175067-A2 biodiversity. 31-MAR-2000; 23-AUG-2000; Drmanac RT, Homo sapiens 13-FEB-2002 11-OCT-2001. AAS69040; 297 237 603 177 663 543 117 723 57 483 RESULT 7 g d ₹ à à dd Ś g à

23-JUN-2000; 2000US-0213588P 20-MAR-2001; 2001US-0276909P

WPI; 2002-114576/15

Morozov V;

Xiao Y,

(FARB) BAYER AG

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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; alterosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Censtmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss; EST; expressed sequence tag.
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polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pot_sequences
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This invention comprises the cDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease purliated from human seminal fluid. An antibody specific control of micro-metastases, autoimmune lesions and renal failure in diagnosis of micro-metastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tunmour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease. (C-g-g-prion protein amyloid plaques of Genstmann-Straussler Syndrome, creuzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease gene provides a therapeutic target of decreasing human prostasin-like serine protease cutyity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic, anyment and inhibit the enzyme activity which may be useful to treat correct particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proflegation and inhibit the progression of restenosis and appropreduced the progression of restenosis and appropriating the progression of restenosis and appropriation and inhibit the progression of restenosis and appropriation and inhibit the progression of restenosis and approached the progression of restenosis.
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                                                                                                                                                                                                                                                                                                                      Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         athercaclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutarions in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #2 nucleotide sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cecededentabacacerredidadadadadadacinacradadadadada
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34.8%; Score 384; DB

Best Local Similarity 100.0%; Pred. No. 4.7

Matches 384; Conservative 0; Mismatches
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356 CICCCAGGACGGGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCAICGTGGTGCC 415

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TITCALGACGAALGGGACGILGGAGCCCGGCCGAGTGGTCGGTACTGCTGGGCGTGCA 341 CTCCCAGGACGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCC 401 TGGCCACATCTGCGGGGGCTCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTG redeckackircrecededecreerckirckireeceercerederecreiceererekerd 162 GGGGGGTCAAACGCGCAGCCGGGCACCTGGCCAAGTGAGCCTGCACCATGAAG SEQ ID NO: 650. 31.4%; 99.7%; 2000JP-00118774. 99JP-00194486 11-JAN-2000; 2000JP-00118774 02-MAY-2000; 2000JP-00183765 AAK92190 standard; cDNA; 670 07~JUL-2000; 2000EP-00114089 Human cDNA 5' -end sequence, 396; Conservative (first entry) genetic manipulation. (HELI-) HELIX RES INST. WPI; 2001-524255/58 Query Match Best Local Similarity 38-JUL-1999; Homo sapiens EP1130094-A2 06-NOV-2001 05-SEP-2001 176 222 236 282 342 296 AAK92190; Best Loca Matches ä RESULT 9 AAK92190 g à Ωp ð 임 ð

Б à 엄 ठ 임 à ö The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Frimers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enrich cDNA. The full ength clones were synthesised by the oligo-capping method. The primers libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the s'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO 221 830 Primers useful for synthesizing full length cDNA clones and their use Gaps Koga H; . Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga Length 670; Claim 2; SEQ ID NO 650; 1380pp + Sequence Listing; English. Human; full length cDNA; cDNA synthesis; oligo-capping; ss. Sequence 670 BP; 97 A; 245 C; 205 G; 118 T; 0 U; 5 Other; 1; Indels Score 346; DB 4; I Pred. No. 2.6e-151; 0; Mismatches 1; GGTGACTCTGGGGGGCCCCTGGTC 24

0 The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in CD-ROM format directly from 830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation. 521 535 0; Gaps CGCCAGCCTGGGCCCCGCCCTGTCTGCCTGCCCCGCGCCTCCACACCGCTTTCGT 476 GGCCAGCCTGGGCCCGCGTGTGGCCTGTCTGCCCCCCGCGCCTCACACCGCTTCGT GGCCAACTACAGCCAAGTGGAGCTGGGCCGGACCTGGCCCTGCTGCCTGGCCTCACC Ħ, Kawai Y; T, Koga Example 11; SEQ ID NO 1916; 1380pp + Sequence Listing; English. Human; full length cDNA; cDNA synthesis; oligo-capping; ss. Sequence 670 BP; 97 A; 245 C; 205 G; 118 T; 0 U; 5 Other; Query Match 31.4%; Score 346; DB 4; Length 67 Best Local Similarity 99.7%; Pred. No. 2.6e-151; Matches 396; Conservative 0; Mismatches 1; Indels Human cDNA clone representative sequence, SEQ ID NO: 1916. Hayashi K, Ishii S, K, Kojima S, Otsuki GCACGGCACCGCCTGCTGGGCCACCGGCTGGGGAGAC 558 Isogai T, a T, Nagai 99JP-00194486. 2000JP-00118774. 2000JP-00183765. 07-JUL-2000; 2000EP-00114089. AAK93456 standard; cDNA; 670 (first entry) Sugiyama (HELI-) HELIX RES INST WPI; 2001-524255/58. Nishikawa T, 08-JUL-1999; 11-JAN-2000; 05-SEP-2001. 02-MAY-2000; Wakamatsu A, Homo sapiens. EP1130094-A2. 06-NOV-2001 522 (AAK93456; 462 402 416 Ľ RESULT 10 AAK93456

162 GGGGGGCTCAAACGCGGCGCGCGCCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGG 221

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521
                                                                                                                                                            Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; peart disease; renal gland disease; mall intestine disease; thymus disease; lymph node disease; macular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; microbial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
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176 GGGGGGCTCAAACGCGGCAGCCGGGCACCTGGCCAAGTGAGCCTGCACCATGGAGG 235
                            TGGCCACATCTGCGGGGGGTCCCTCATCGCCCCTCCTGGGTCCTCCCGCTGCTCACTG 281
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The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polymucleotides are useful for treating nervous and polymucleotides are useful for treating nervous and mescular diseases, for inhibiting tumour formation and metastasis, for treating apartrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, colon, for treating lippase deficiency in cystic fibrosis and colon, for treating lippase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation such as myocardial pancreation, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating liver diseases, coagulation discorders and microbial diseases, for treating immune disorders, for treating inflammation and transplant rejection, for enhancing bone transplant rejection, for enhancing bone thickness and increasing apoptosis, and for regulating vascular ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 ATCGTGGGGGGCTCAAACGCGCAGCGGGGCACCTGGCCAAGTGAGCCTGCACCTA 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GGAGGIGGCCACATUTGCGGGGGCTCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCT
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 Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immut disorders, microbial diseases, inflammation and transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 135; DB 4; Length 768; 100.0%; Pred. No. 9e-53;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 768 BP; 125 A; 280 C; 224 G; 139 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #6883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                              Claim 2; Page 44-45; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS71079 standard; cDNA; 2298
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTGTTTCATGACG 291
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Best Local Similarity 100.
Matches 135; Conservative
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed considerable. (II) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and (II) and (II) are useful for treating disorders of supplement protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Aas&4497-AAS$94564 represent novel human diagnostic coding sequences. Aas&4497-AAS$94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this contine the printed specification, but was obtained in the print of the contine of the
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                     Claim 1; SEQ ID NO 6883; 103pp; English
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Best Local Similarity 100.
Matches 135; Conservative
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21-JUN-2001; 2001US-0300159P. 27-JUN-2001; 2001US-0301351P.

(MILL-) MILLENNIUM PHARM INC.

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                                                                                                                              The invention comprises a method for assessing whether a patient is afflicted with breast cancer or ovarian cancer. The method involves the use of specific DNA markers. The method of the invention is useful in the detection and treatment of ovarian and breast cancer. DNA sequences ABT31894 - ABT31949 encode human breast/ovarian cancer-related proteins
                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a variety of markers.
                                                                                                                                                                                                                                                                                                 1 GGGCCCTTGTCCTGGGCCATGGCCCAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCT
                                                                                                                                                                                                                                                                       Gaps
                                                        Determining the presence of breast cancer in an individual, involves using specific polynucleotide markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian cancer; identification; detection; characterisation; tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of ovarian cancer, of a variety of ma
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                                                                                                                                                                                                               Sequence 1733 BP; 311 A; 578 C; 500 G; 344 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          Length 1733;
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0, 5e-21; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian cancer cell expressed sequence 10798.
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                                                                                                                                                                                                                                             ch 6.1%; Score 67; DB 1 Similarity 100.0%; Pred. No. 5e-67; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1001-1002; 1198pp; English.
                                                                                                      Disclosure; Page 192-193; 233pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF98698 standard; DNA; 1796 BP.
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2000US-0190347P.
2000US-0191321P.
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                                                                                                                                                                                                                                                                                                                                                             GIGGCCA 67
                          2003-267848/26.
                                                                                                                                                                                                                                                               Local Similarity
                                       P-PSDB; ABJ37067
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21-MAR-2000;
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20-JUL-2000;
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Veiby OP;
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AAF98698
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The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see AAF98594 to AAF98730), in a patient sample, and (2) the mornal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. It have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer
where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (I) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (I) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                               134 descectificatectigaceardseceaaadagaarieeragagaeeragaacardagaactificadagaari 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection, assessment, prevention and therapy of ovarian cancer, comprises detecting changes in the expression of a variety of markers.
                                                                                                                                                                                                                                                                                                           1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ovarian cancer; identification; detection; characterisation; tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
                                                                                                                                                                                           Sequence 1796 BP; 327 A; 599 C; 511 G; 359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                   Length 1796;
                                                                                                                                                                                                                     o. 5e-21; 0; Indels
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                                                                                                                                                                                                                                                       1 Similarity 100.0%; Pred. No. 5e-67; Conservative 0; Mismatches
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                                                                                                                                                                                                                                     Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF98720 standard; DNA; 1835 BP.
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16-MAR-2000; 2000US-0190347P.
21-MAR-2000; 2000US-0191321P.
31-MAX-2000; 2000US-020382P.
20-JUL-2000; 2000US-00220467.
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                                                                                                                                                                                                                                                                               Matches
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assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
                                                                                                                                    Gaps
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                                                                                                      Length 1835;
                                                                   Sequence 1835 BP; 309 A; 621 C; 527 G; 378 T; 0 U; 0 Other;
                                                                                                                                    Indels
                                                                                                   Score 67; DB 5;
Pred. No. 5e-21;
                                                                                                                 100.0%; Pred. No.
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Job time: 478 secs
                                                                                                                                       67; Conservative
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BX436299 BX436299
AA300017 EST12620
                                                 February 25, 2004, 12:18:11; Search time 2783 Seconds (without alignments) 11824.694 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                      27513289 seqs, 14931090276 residues
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                                    nucleic search, using sw model
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ALIGNMENTS

O'THE AW450407

MAGE: 2735037 3', MRNA sequence.

INA AW450407

MAGE: 2735037 3', MRNA sequence.

MAGE: 27350407 11 111, Gov.

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MAGE: 27350407 11 111, Gov.

MAGE: 27350407 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (Dases 1 to 456) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
106 CTCTCCAGAIATTGCCAGAGATGCTGTGTGCTGGCTACCCAGAGGGCCGCAGAGGACACCT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ggapbs-r@mail.nih.gov
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 712 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 452.
Location/Qualifiers
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34.8%; Score 384; DB 9; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.6e-170;
Matches 384; Conservative 0; Mismatches 0; Indels
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AI190509.1 GI:3741718
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Unpublished (1997)
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/dlone="IMAGE:2735037"
/lab host="UMAGE:2735037"
/lab host="UMAGE:2735037"
/lab host="UMAGE:2735037"
/lab host="UMAGE:2735037"
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/note="Vector: pT7735-Pac (Pharmacia) with a modified
/note="CGAP Sub5 library derived from NCI CGAP Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3662-3683, 3799-3803 (IMAGE CloneIDs
// NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
// NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
// NCI CGAP CloneIDs 1225912-1427693,
// NCI CGAP CLONEIDS
// NCI CGAP PAC 2 pool 1 LLAM 2457-2459, 2758-2759,
// NCI CGAP PAC 2 pool 1 LLAM 2457-2459, 2758-2759,
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// NCI CGAP PAC 2 pool 0 f 3,840 arrayed clones from the driver population), plus a pool of 11,136 clones from driver population), plus a pool of 5,472 clones from driver population), plus a pool of 5,7259-272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 CCCGCGCAGTGGCCGCCCAACTACAGCCAAGTGGAGCTGGGCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=colon
TAG_LIB=NCI_CGAP_Col0
TAG_SEQ=AAACG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local
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DEMARDIAGE

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CE

Hoses I to 294)

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

CE

Hoses I to 294)

Radams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldmer, R.A.,

Bult, C.J., Lee, N.H., Kirknes, B.F., Weinstock, K.G., Gocayne, J.D.,

Bult, C.J., Lee, N.H., Kirknes, B.F., Weinstock, K.G., Gocayne, J.D.,

Rolley, C. Chine, T.R., Cotton, M.D., Earle-Hughes, J., Fire, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Rolley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hustings, G.A.,

Raymond, L., Wei, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence

M. Dakues 377 (6547 Suppl), 3-174 (1995)
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Seq primer: M13 Reverse.
                                                                                                                                                                                EST 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 geoccerrorcingoccarrescendanagegerecreegecergegere
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294 bp mRNA linear EST 18-7
EST12620 Uterus tumor I Homo sapiens CDNA 5' end similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
The Institute for Genomic Research
The Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Best Local Similarity 100.0%; Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other ESTs: EST12621 THC176739
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 3018699423
Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                prostasin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  AA300017.1 GI:1952347
226 AAGACCCAGTCAGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GIGGCCA 67
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PUBMED
COMMENT
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ORGANISM
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/tissue type="THYMUS"
/tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Woctor: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was digested with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and SCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 TTTGGCTGTGGACGGAGAAACCGCCTGGAGTTTTCACTGCTGTGGCTACCTATGAGGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 İGGATACGGGAĞCAĞGTĞATĞĞĞTİÇAĞAĞCCTĞĞĞCCTĞCCTTTCCCACCGAGCCCAĞ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX436299 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YG17 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamanla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                 679 CAGATATTGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGCCGCAGGGACACCTGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact
Feng biang Bmail: fliang@lifetech.com WEL:
http://fullnength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001AD09FM1.
Location/Qualifiers
                                                                                                                                                        678
                                                                                                                                                                                                                                                                                                                                  84 CAGATATTGCCAGGGATGCTGTGTGTGCTTACCTACCCAGAGGGCCGCAGGGACACCTGCCAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope. Centra National de Sequencage
BP 191 91006 Echtra Cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Inbrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7995.f For
more information about this cluster, see
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                                                                     CTGGGCGAGGCCACCTGTCAATGTCTCTACAGCCAGCCCGGTCCCTTCAACCTCACTTC
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llarity 100.0%; Pred. No. 1.4e-52;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               739 GGTGACTCTGGGGGGCCCCTGGTC 762
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us-10-037-417-45.oli.rst

DEFINITION

RESULT 5 BM828821

ACCESSION

VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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/ organism="Homo sapiens"
// organism="Homo sapiens"
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// not lib="Lb="Mth a Not I; Site 2: Eco RI; lst strand cDNA
polylinker; Site 1: Not I; Site 2: Eco RI; lst strand cDNA
was primed with a Not I = oligo(dr) primer [5'
was primed with a Not I = oligo(dr) primer [5'
youble-stranded cDNA was ligated to Eco RI
T 3 / ; double-stranded cDNA was ligated to Eco RI
T 3 / ; double-stranded cDNA was ligated to Bco RI
the Not I and Eco RI sites of the modified pr773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Guencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/lange/image.html
Innert Length: 691 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 334.
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tg25f08.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109831 3'
similar to SW:PSS8_HUMAN Q16651 PROSTASIN PRECURSOR ;, mRNA
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1 (bases 1 to 360)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thumor Gene Index Unpublished (1997)
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Best Local Similarity. 100.0%; Pred. No. 1.9e-20;
Matches 67; Conservative 0; Mismatches 0;
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A1393077.1 GI:4222624
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/cell type="Spithelial"
/cell type="Spithelial"
/cell type="Spithelial"
/lab host="Toplor"
/lab host="To
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Xim, Y.S.

21C Frontier Korean EST Project 2001
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K-EST0101694 S9SNUG01 Homo sapiens CDNA clone S9SNUG01-51-E07 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: Kim YS
Contact: Kim YS
Genome Research Center
Genome Research Linstitute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4440
Fax: +82-42-860-4409
Email: yongsungemail.kribb.re.kr
Plate: 51 row: E column: 07
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tive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="S9SNU601-51-E07"
/sex="M"
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Location/Qualifiers
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Homo sapiens
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                                                                                                                                                                                                                                                                          MRNA sequence.
                             218 GTGGCCA 224
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09

Homo sapiens (human)

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Homo sapiens (human)
Unpublished (1997)
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    JOURNAL
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                               COMMENT
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                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.

Emmert-back, M.D., Ph.D.

EDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CAPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 630 Std Error: 0.00

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Bright and Library Std Error: 0.00

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NCI CGAP_PR28"
/clone_lib="NCI CGAP_PR28"
/note="Organ: prostate; Vector: pr773D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pr773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP_PR22 was prepared, and 8s
circles wase made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
c 5,000 clones made from the same library (cloneIDs
985608-986756, 1101192-11011959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammolia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 377)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 366)
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                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2254401"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="adult"
/lab_host="DH10B"
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AI193435.1 GI:3744644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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                               Homo sapiens
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AI193435
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                                                                                                                       AUTHORS
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/ dev stage="19 weeks" / lab_bost="bullook" | dev stage="19 weeks" / lab_bost="bullook" | dev stage="10 weeks" / lab_bost="bullook" | dev stage="10 weeks" / lab_bost="bullook" | decor: pTyT3D (Pharmacia) with a note="Organ: lung; Vector: pTyT3D (Pharmacia) with a modified polylinker; Site=1: Not I; Site=2: Eco RI; lst modified polylinker; Site=1: Not I; -0.1go(dT) primer strand cDNA was primed with a Not I - 0.1go(dT) primer strand cDNA was size selected, ligated to Eco RI double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTyT3 vector (Pharmacia). Library went through one round of for normalization to a Cot = 5. Library constructed bears and M. Fatina Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDHH19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 406)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, S. and
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 bp mRNA linear BST 28-JAN-2003
K-EST0161920 L7N800102 Homo sapiens CDNA clone L7N800102-4-C01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is a vailable royalty-free through Linn, ; contact the

This Clone is a vailable royalty-free through Linn, ;

INAGE Consortium (info@image.linl.gov) for further information.

Insert Length: 763 Std Error: 0.00
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52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 6.1%; Score 67; DB 9; Length 377; 1 Similarity 100.0%; Pred. No. 1.9e-20; Indels 67; Conservative 0; Mismatches 0; Indels
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: C column: 01
High quality sequence stop: 406.
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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1. .377
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CB116948.1 GI:27942755
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0; Gaps

9

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / organism="Homo sapiens"

/ organism="Homo sapiens"

/ db_xref="mxNn"

/db_xref="mxNn"

/db_xref="mxNn"

/db_xref="mxNn"

/db_bost="logo="colon tumor, RER+"

/clone_lib="MYCI CGAP_Col6"

/clone_lib="MYCI CGAP_Col6"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a notified polylinker; Site 1: Not I; Site 2: Ecc RI; modified polylinker; Site 1: Not I; Site 2: Ecc RI; modified polylinker; Site 1: Not I; Site 2: Ecc RI; prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive purification, this DNA was used as tracer in a subtractive hybridization reaction. The diver as PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 105741e-106125; and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A1343968 462 bp mRNA linear EST 08-APR-1999 tc01d05.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:2062569 3' similar to TR:Q16651 Q16651 PROSTASIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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           /dev_stage="adult"
/clone lib="male adult skin, full-length enriched
chimpanzee cDNA library"
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                                                                                                                                              DB 9; Length 409; 2e-20;
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                                                                                                                                                 ch 6.1%; Score 67; DB 1 Similarity 100.0%; Pred. No. 2e-67; Conservative 0; Mismatches
/tissue_type="skin"
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AI343968.1 GI:4081174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                             273 Greecen 279
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                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                  Query Match
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COMMENT
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TITLE
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AI343968
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                                                                                                                                                               / Jab Judge-1.094.ve
//clone lib="LYN800102"
//clone lib="Dry80102"
//note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
Site 2: Not1; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (BAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dr-selected mRNA by
priming with dr-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
Circularized with E. coli DNA ligase after digestion of
converted to a DNA strand by Okayama Berg method. The
competent cells E. coli Toplüf' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakate, R., Osada, N., Hida, M., Sugano, S., Hayasaka, I., Shimohira, N., Yanagi, S., Suto, Y., Hashimoto, K. and Hirai, M. Analyais of 5'-end sequences of chimpanzee cDNAs Genome Res. 13 (5), 1022-1026 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
1 (bases 1 to 409)
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AU29808 male adult skin, full-length enriched chimpanzee cDNA
Library Pan troglodytes verus cDNA clone PstA2814 5' similar to
human Refseq mRNA NM_002773, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Integrated Biosciences
The University of Tokyo, Graduate School of Frontier Sciences
5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan
Tel: 81-4-7136-3688
Fax: 81-4-7136-3687
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/mol type="mRNA"
/sub_species="verus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 67; DB 14; I. 100.0%; Pred. No. 1.9e-20; tive 0; Mismatches 0;
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/clone="PstA2814"
                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N800102-4-C01"
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Location/Qualifiers
                                                                                                                                                         'lab_host="Top10F
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RESULT 13
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Insert Length: 601 Std Error: 0.00
Seq primer: -40UP from Gibco
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1 (bases 1 to 472)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                        GGGCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCT
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Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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6.1%; Score 67; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 67; Conservative 0; Mismatches 0; Indels
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/db xref="taxon:9606"
/clone="1MAGE:2394723"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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AI761519.1 GI:5177186
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Bukaryota, Metazoa, Chordates, Catarrhini, Hominidae, Pan.
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Pan.
Chaese 1 to 479)
Sakate, R., Osada, M., Hida, M., Sugano, S., Hayasaka, I., Shimohira, N., Yanagi, S., Suto, Y., Hashimoto, K. and Hirai, M.
Analysis of 5'-end sequences of chimpanzee cDNAs
Genome Res. 13 (5), 1022-1026 (2003)
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1 (bases 1 to 479)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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479 bp mRNA linear EST 08-MAY-2
AU298317 male adult skin, full-length enriched chimpanzee cDNA
library Pan troglodytes verus cDNA clone PstA5634 5' similar to
human RefSeq mRNA NM_002773, mRNA sequence.
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Department of Integrated School of Frontier Sciences
The University of Tokyo, Graduate School of Frontier Sciences
5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan
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/clome lib="male adult skin, full-length enriched
chimpanzee cDNA library"
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AGENCOURT 13621004 NIH MGC_148 Homo sapiens cDNA clone
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.1%; Score 67; DB Best Local Similarity 100.0%; Pred. No. 2e-Matches 67; Conservative 0; Mismatches
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/sub_species="verus"
/db_xref="taxon:37012"
/clone="PstA5634"
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Fax: 81-4-7136-3687
Email: mhirai@k.u-tokyo.ac.jp.
Location/Qualifiers
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213 GTGGCCA 219
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Best Local Similarity
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Matches
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cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.G.E. Consortium/Link, send email to:
info@image.llnl.gov
Seq primer: -40UP /rom Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF063417 10 CGAP CO16 Homo sapiens CDNA clone IMAGE:3323178 3' similar to SW:PSSE_HUMAN Q16651 PROSTASIN PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM346 row: p column: 21

High quality Sequence stop: 478.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                   /tissue type="pre-eclamptic placenta"
/lab host="DH10B TonA"
/clone lib="WIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-Xho1; Site 2: BamH; Library is oligo-dr primed and directionally cloned using primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGGCAAGTGGGGGCT
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Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 67; DB 14; Length 479; 100.0%; Pred. No. 2e-20; 1.ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                            'clone="IMAGE:30331484"
                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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BF063417.1 GI:10822327
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Unpublished (1997)
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Matches 67; Conservative
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KEYWORDS
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Source | ...492
| Jurganism="Homo sapiens" |
| And xacf="taxon:9606" |
| And xacf="taxon:9606" |
| Ala xacf="taxon:9606" |
| Arisaue_type="colon tumor, RER+" |
| Alab host="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE-"TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE="TAMGE-"TAMGE="TAMGE="TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMGE-"TAMG
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TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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LENGTH: 610
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                                                                          2004, 12:20:46; Search time 110 Seconds (without alignments) 5559.599 Million cell updates/sec
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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3. /cgn2_6/ptodata/2/ina/seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-280-116-29

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US-09-020-956-120

US-09-020-956-120

US-09-020-956-120

US-09-32-616A-120

US-09-32-616A-120

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US-09-685-166A-120

US-09-685-166A-139
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RESULT 2
US-09-280-116-28/C
US-09-280-116-28/C
Sequence 28, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REPRENCE: 5800-24, 035800/176965
CURRENT PILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PATENTING DATE: 1999-03-26
SOFTWARE: PATENTING DATE: 2099-03-26
SOFTWARE: PATENTING DATE: 340
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 0.082;
iive 0; Mismatches 0
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US-09-030-607-175
US-09-439-313-175
US-09-352-616A-175
US-09-159-812-175
US-09-159-812-175
US-09-685-166A-175
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US-09-685-166A-175
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US-09-494-921-28
US-09-494-921-29
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                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09280116A Patent No. 6331427 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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731 CCTGCCAGGGTGACTCTGGGGG 752
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                             Sequence 7, Application US/09386642
Patent No. 6420157
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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EDNESS: single
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STATE: WA
                                                                                                                                                                                                                                                                           SEQ ID NO 7
LENGTH: 1169
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RESULT 5
US-09-386-642-7
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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US-09-280-116-29/C
Sequence 29, Application US/09280116A
Sequence 29, Application US/09280116A
PERCENT NO. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE PARENT OF SEQ ID NOS: 268
SOFTWARE PARENT OF SEQ ID NOS: 268
SOFTWARE PARENT OF SEQ ID NOS: 268
TRAGIH: 340
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                                                                                                      Gaps
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2.1%; Score 23; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                        ch 2.1%; Score 23; DB 4; Length 340;
1 Similarity 100.0%; Pred. No. 0.25;
23; Conservative 0; Mismatches 0; Indels
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; CTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-29
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Sequence 8, Application US/09386642;
Patent No. 6420157;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028;
CURRENT APPLICATION NUMBER: US/09/386,642;
CURRENT FILING DATE: 1999-08-31;
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 4;
Pred. No. 0.69;
0; Mismatches
      OTHER INFORMATION: trypsin-like serine proteases
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100.0%; Pre
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Matches 22; Conserv
                                                                       Query Match
Best Local Similarity
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LENGTH: 1142
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US-09-386-642-8
                ; OTHER INFURM
US-09-280-116-28
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Sequence 120, Application US/09020956
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Sequence 120, Application US/09020956
GENERAL INFORMATION:
APPLICANT: Xu, Janachun
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APPLICANT: Xu, 
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0.69;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.0%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 22; Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFANCE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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patent No. 6395278

patent Normanian Harlocker, Sugan Louise

papticant: Dillon, Davin C.

papticant: Jiang, Vuqui

papticant: W. Jiangchun

papticant: Xu, Jiangchun

papticant: Xu, Jiangchun

papticant: Xu, Jiangchun

papticant: No. 95 PROSTATE CANCHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCHER AND METHODS FOR THEIR USE

TITLE OF INVENTION: OF PROSTATE CANCHER AND METHODS FOR THEIR USE

CURRENT FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SOFTWARE: FastSEQ for Windows Version 3.0

seq ID NO 120

LENGTH: 90

LENGTH: 90
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                                        APPLICANT: Fanger, Gary
APPLICANT: Fanger, Mark
APPLICANT: Relter, Mark
APPLICANT: Bolk, John
APPLICANT: Bolk, John
TITLE OF INVENTION: COMPOSITIONS AND NETHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: UNBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
EBNGTH: 90
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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
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US-09-232-149A-120/c
Sequence 120, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
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NAME/KEY: misc_feature
NAME/TON: (1)...(90)
OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-120
Reed, Steven G.
Kalos, Michael
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Pred. No. 2.2;
tive 0; Mismatches 0; Indels
                                               1.9%; Score 21; DB 3; Length 90;
100.0%; Pred. No. 2.2;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin R2-ase #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: MAK: David J.
NAME: MAK: David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/09/030,607
25-FEB-1998
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Patent No. 6329505
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
                                                                                                                                               739 GGTGACTCTGGGGGGCCCCTG 759
                                                                                                                                                                                                                                                                                                      Sequence 120, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
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, ORIGINAL SOURCE:
, ORGANISM: Homo sapiens
US-09-030-607-120
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Matches 21; Conservative
                                                           Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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                US-09-020-956-120
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Query Match
1.9%; Score 21; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches
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; Sequence 120, Application US/09685166A
; Patent No. 6630305
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NAME/KEY: misc_feature
LOCATION: (1)...(90)
OTHER INFORMATION: n = A,T,C or G
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Vedvick, Thomas S.
Carter, Darrick
                                                                                Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Kalos, Michael D.
                    Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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ORGANISM: Homo sapien
                                                                                                                                                     Li, Samuel
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LENGTH: 90
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APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:

APPLICANT: Xu, Jangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF

TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.428C5

CURRENT APPLICATION NUMBER: US/09/159,812A

CURRENT FILING DATE: 1998-09-23

NUMBER OF SEQ ID NOS: 306

SEQ ID NO 120

LENGTH: 90

LENGTH: 90
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         APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 120
LENGTH: 90
LENGTH: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 120, Application US/09159812A
Patent No. 6613872
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; OTHER INFORMATION: n = A,T,C or G
US-09-159-812-120
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; CTHER INFORMATION: n = A,T,C or G
US-09-232-149A-120
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ORGANISM: Homo sapien
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US-09-159-812-120/c
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
FILE REFERENCE: 220011.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-115-453-120/c

US-09-115-453-120/c

Sequence 120, Application US/09115453B

Patent No. 6657056

GENUERL INFORMATION

APPLICANT: W. Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

TITLE OF INVENTION: METHODS FOR THEIR USE

PILE REPERENCE: 210121.427C4

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

CURRENT FILING DATE: 1980-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 120

LENGTH: 90
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APPLICANT: Dillon, Davin C.
APPLICANT: Milchan, Jennifer Lynn
APPLICANT: Milchan, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LA1012.
TITLE OF INVENTION: 201011.3/09/688,489
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 90
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1.9%; Score 21; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                     Query Match 1.9%; Score 21; DB 4; Length 90; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 21; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc feature
LOCATION: (1)...(90)
CTHER. INFORMATION: n = A,T,C or G
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) LOCATION: (1)...(90)

; OTHER INFORMATION: n = A,T,C or G

US-09-115-453-120
, OTHER INFORMATION: n=A,T,C or G US-09-685-166A-120
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ORGANISM: Homo sapien
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Search completed: February 25, 2004, 14:37:33 Job time : 111 secs

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Sequence 10, Appl
Sequence 21306, A
Sequence 65, Appl
Sequence 847, Appl
Sequence 29, Appl
Sequence 214, Appl
Sequence 11, Appl
Sequence 141, Appl
Sequence 141, Appl
Sequence 931, Appl
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-029-386-21306
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: WHYTE, DAULD
APPLICANT: CARNEDEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSAMM, SUCRA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 60/214,047
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 52
SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 716; ]
Pred. No. 0;
                                                                                                               Sequence 52, Application US/0988615 Patent No. US20020064856A1
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APPLICANT: PLOWMAN, GREGORY
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Best Local Similarity 99.8
Matches 816; Conservative
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ORGANISM: Homo sapiens
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RESULT 1
US-09-888-615-52
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Bavid R.
APPLICANT: Hankel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS IWO
TITLE OF INVENTION: EXPRESSION ANALYSIS IWO
FILE REFERENCE: AEONICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21306
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                                                                                                                                                                                                                                                                                                                                                                     217 GGAGGIGGCCACAICIGCGGGGGCTCCCTCAICGCCCCCTCCTGGGTCCTCTCCGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                  157 ATCGTGGGGGCTCAAACGCGCAGCCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCAT
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OTHER INFORMATION: MAP TO CHRI6.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN ENTAL LIVER, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6

OTHER INFORMATION: WILSPROT HIT: 9114779472, EVALUE 0.000e+00

OTHER INFORMATION: SMISSPROT HIT: Q1651, EVALUE 0.000e+00

US-10-029-386-21306
                                                                                                                                                                   Query Match
12.3%; Score 135; DB 14; Length 768;
Best Local Similarity 100.0%; Pred. No. 6e-59;
Matches 135; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
6.1%; Score 67; DB 14; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-24;
Matches 67; Conservative 0; Mismatches 0; Indels
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21306, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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; Sequence 7606, Application US/10029386
; Publication No. US20030194704A1
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                                                                              TYPE: DNA ORGANISM: Homo sapiens
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                            SEQ ID NO 10
LENGTH: 768
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     CCGCGGCCCGAGTGGTTCCTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGACGGCC
                                                                                                                                                                                     CGCACACCCCCCCATCGTGGTGCTGCTGCCCAACTACAGCCAAGTGGAGCTGG
                                                                                                                                                                                                                                                                                    GCGCCGACCTGGCCCTGCCTGCCCTCACCCGCCAGCCTGGGCCCCCGCCGTGTGGC
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US-10-221-097-10
Sequence 10, Application US/10221097
Publication No. US20030144476A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Panka)
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Winny, Zhaoying
ITILE OF INVENTION: NOVEL COMPOUNDS
ITILE OF INVENTION: NOVEL COMPOUNDS
ITILE OF INVENTION: NOVEL COMPOUNDS
ITILE OF INVENTION: NOVEL CONDOUNDS
FILE REFRENCE: 2020-09-06
CURRENT FILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                             368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gagcccrrgrcraggccargecccagaagaggrccrggggccrggggagcrgggggcr
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                                                                                                                                                                                                          APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SUFTWARE: Patentin Ver. 2.1
LENGTH: 3382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Pred. No. 4e-24;
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100.0%; Pred. No....
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/042,865
                                                                          ; Sequence 447, Application US/10101510; Publication No. US20030148295A1; GENERAL INFORMATION: APPLICANT: WAN, JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/10042865 Publication No. US20040029216Al GENERAL INFORMATION:
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Grosse, William M
Alsobrock II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Blerman, Karen
MacDougall, John
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Gasman, Stacie J
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly
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Gangolli, Esha A
Burgess, Catherine E
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Vernet, Corine A.M
Taylor, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tchernev, Velizar
Miller, Charles E
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smithson, Glennda
Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-101-510-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 driedeck 278
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                                                     US-10-101-510-447
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                     APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 7606
LENGTH: 543
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Sequence 85, Application US/10176847

Sequence 85, Application US/10176847

Publication No. US20030068636A1

REBURGAL INFORMATION:

APPLICANT: Veiby, Petter Ole

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST;

TITLE OF INVENTION: AND OVARIAN CANCER

FILE REFERENCE: MRI-039

CURRENT APPLICATION NUMBER: US/10/176,847

CURRENT FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FRRESEQ for Windows Version 4.0
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: ST HUMAN HIT: Q1442128.1, EVALUE 7.00e-04
OTHER INFORMATION: NT HIT: U33446.1, EVALUE 0.00e+00
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Best Local Similarity 1000.
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Best Local Similarity
Matches 67; Conservat
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SENERAL INFORMATION:
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US-09-967-768A-141
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US-09-967-768A-141
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US-10-097-340-261
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Patent No. US20020090625A1
GENERAL INFORMATION
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Work, Samuel
APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
FILE REFERENCE: 81994/282423
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APPLICANT: Horne, Useph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REPERENCE: 44921-5028-WO
CURRENT APPLICATION UNDER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
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Best Local Similarity 100.0%; Pred. No. 6.7e-17;
Matches 53; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. c.
... 0; Mismatches
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CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
LENGTH: 1834
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-8
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 29
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. Sequence 2214. Application US/09880107
. Patent No. US20020142981A1
. GENERAL INFORMATION:
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; LOCATION: (229)..(1260)
US-09-948-094-1
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ORGANISM: Homo sapiens
FEATURE:
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CORGANISM: Homo sapiens
US-10-042-865-29
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US-09-948-094-1
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Best Local S
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| Sequence 14.1, Application US/09967768A|
| Sequence 14.1, Application US/09967768A|
| Patent No. US20020150877A|
| GENERAL INFORMATION:
| APPLICANT: Augustus, Meena |
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu |
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu |
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu |
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu |
| TITLE OF INVENTION: Sets |
| FILE REFERENCE: 689290-72 |
| FILE REFERENCE: 689290-72 |
| FILE REFERENCE: Cancer Gene Determination and Therapeutic Screening Signatu |
| FILE OF INVENTION: Sets |
| FILE OF INVENTION NUMBER: US/60/236,109 |
| PRIOR FILING DATE: 2000-09-28 |
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US-09-880-107-2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4.8%; Score 53; DB 9; Length 1834; 100.0%; Pred. No. 6.7e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1834;
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100.0%; Pred. No. 6.7e-1
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFWARE: Patentin Ver. 2.1
LENGTH: 1934
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Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Schastian HOERSCH
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peter VEIBY
Gordon B. MILLS
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                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Matches 53; Conserv
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Best Local Similarity
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US-09-922-217-931

APPLICANT:

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Sequence 931, Application US/09833263
; Sequence 931, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Alin
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Clapper, John A.
; APPLICANT: Clapper, John A.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 21011.471C12
; CURRENT APPLICATION NUMBER: US/09/833, 263
; CURRENT PILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SEQ ID NO 931
; LENGTH: 596
                                                                                                             Gaps
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CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
                                                                                                                                                                    1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCCAG
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                                                      Length 596;
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4.6%; Score 51; DB 9; Length 596
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                             Indels
                                                      Query Match
'4.6%; Score 51; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-025-380-931/c

| Sequence 911, Application US/10025380 |
| Publication No. US20020182191A1 |
| GENERAL INPORMATION: |
| APPLICANT: Xu, Jiangchun |
| APPLICANT: Lodes, Michael J. |
| APPLICANT: Benson, Darin R. |
| APPLICANT: Benson, Darin R. |
| APPLICANT: Stolk, dohn A. |
| APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

LCCATION: (1)...(596)

CTHER INFORMATION: n = A,T,C or G

US-09-833-263-931
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
Clapper, Jonathan D.
Skeiky, Yasir A. W.
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Vedvick Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                         US-09-833-263-931/c
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                                                               APPLICANT: Xunei ZHAO
APPLICANT: Xunei ZHAO
APPLICANT: Xunei ZHAO
APPLICANT: Xunei ZHAO
APPLICANT: Xunei ZHAO
APPLICANT: Xunei ZHAO
TITLE OF INVENTION: Nacleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT PLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-09-26
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APPLICANT: Smith, Carcle Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
ATILE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.8%; Score 53; DB 14; Length 1834; Best Local Similarity 100.0%; Pred. No. 6.7e-17; Matches 53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 261 LENGTH: 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 931, Application US/09922217
Patent No. US20020076414A1
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Stolk, John A.
Wang, Tongtong
Robert C. BAST, Jr.
Karen LU
                                                 Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
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ORGANISM: Homo sapiens
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LENGTH: 596
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APPLICANT:
APPLICANT:
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Search completed: February 25, 2004, 15:44:57 Job time: 457 secs
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APPLICANT: Zhong Mei
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APPLICANT: Burgess, Catherine E
APPLICANT: Burgess, Catherine E
APPLICANT: Burgess, Catherine E
APPLICANT: Patiung and Mei
APPLICANT: Taylor, Sarah
APPLICANT: Taylor, Sarah
APPLICANT: Taylor, Sarah
APPLICANT: Grose, William M
APPLICANT: Grose, William M
APPLICANT: Grose, William M
APPLICANT: Reinger, Shlomit R
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APPLICANT: Reinger, Shlomit R
APPLICANT: Malyarar, Criel M
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APPLICANT: Shlomin Raren
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APPLICANTON NUMBER: 60/274,876
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APPLICANTON NUMBER: 60/274,876
APPLICANTON NUMBER: 60/274,876
APPLICANTON NUMBER: PatentIn Ver. 2.1
APPLICANTH: 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCCCTTGTCCTGGGCCCAGAAGGGGGTCCTGGGGCTGGGCAG 51
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4.6%; Score 51; DB 13; Length 596;
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 51; Conservative 0; Mismatches 0; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 931 LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/10042865; Publication No. US20040029216Al.
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
                                                                                                                                         FEATURE:

NAME/KEY: misc_feature

LOCATION: 538

CTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zerhisen, Bryan D
Zerhisen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
snvtek, Kimberly
                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-042-865-31
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APPLICANT:
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Gaps
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                                                                                          Query Match
4.4%; Score 49; DB 12; Length 1161;
Best Local Similarity 100.0%; Pred. No. 8.1e-15;
Matches 49; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                      19 ATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCTGTGGCCA
                    ; ORGANISM: Homo sapiens
US-10-042-865-31
TYPE: DNA
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February 25, 2004, 14:35:42; Search time 100 Seconds (without alignments) 1008.695 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                                                                                                                           Sequence:
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geneseqn1990s:*
geneseqn2000s:*
geneseqn2001s:*
geneseqn2001s:*
geneseqn2003s:*
geneseqn2003bs:*
geneseqn2003bs:*

A_Geneseq_29Jan04:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abb09524 Human pro	Human	Human	Amino	Aam93568 Human pol	Human	Novel	Abg96402 Human ova	Human	Amino	Human	Human	Human	Human	Abg72018 Mouse cha		Abp61011 Novel hum		Abp61010 Novel hum	Abg91414 Primate L	Aau00467 Human ser			Aag67514 Amino aci	Abb07284 Human pro
SUMMARIES	ID	ABB09524	ABB09523	ABB98135	AAU82753	AAM93568	AAU75082	ABG04853	ABG96402	AAU78547	ABB07285	ABJ37067	ADD47565	ADD47561	ABB98415	ABG72018	ABB98416	ABP61011	ABB07286	ABP61010	ABG91414	AAU00467	AAU74748	AAE14348	AAG67514	ABB07284
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	Length	357	344	818	818	766	178	198	343	343	343	343	343	343	307	339	386			280	280	284	346	691	255	262
	Match	100.0	0.96	77.1	77.1	61.5		41.2	35.3	35.3	35.3	35.3	35.3	35.3	33.0	32.1	31.3	30.4	0	30.2	0	30.2	29.8	•	29.5	29.4
	Score	1953	1874	1505	1505	1202	970	804.5	069	069	069	069	069	069	645	627.5	612	593.5	590	590	590	590	582.5	582	575.5	574
Result	No.	н	7	м	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Li L;

Tchernev VT, Liu X, Spytek KA; Lepley DM, Burgess CE, Vernet CAM,

Kekuda R, Alsobrook JP, ' Patturajan M, Grosse WM,

(CURA-) CURAGEN CORP.

•	Aam41174 Human pol		Aaw77304 Amino aci	Aay73388 HTRM clon	Aau12282 Human PRO	Aab73945 Human pro	Aae03821 Human gen	Abg64545 Human alb	Novel	Abu80980 Human PRO	Abu66680 Human PRO	Abu59761 Novel sec	Abo24951 Human sec	Abg73394 Human ser		Ada45741 Novel hum	Ada76172 Human PRO	Ada18822 Human PRO		Adb19230 Novel hum	
	AAM41174	AAU75907	AAW77304	AAY73388	AAU12282	AAB73945	AAE03821	ABG64545	AB017726	ABU80980	ABU66680	ABUS9761	AB024951	ABG73394	ABU66956	ADA45741	ADA76172	ADA18822	ADA61445	ADB19230	
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	328	389	297	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	
	29.1	29.0	29.0	28.8	28.8	28.8	28.8	80	28.8	28.8	28.8	28.8	8	28.8	28.8	28.8	28.8	ω,	28.8	28.8	
	568.5	567	266	563	563	563	563	563	563	563	563	563	563	563	563	563	563	563	563	563	
	26	27	28	29	30	31	32	33		3.5	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Human; NOVX; neurological disorder; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;

W thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

KW thyroiditis; incontinence; psoriasis; scleroderma; alopecia;

KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW metabolic pathway regulation disorder; oytostatic; neuroprotective;

KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

KW defiferentiation; proliferation; motility; heamatopoiesis; wound healing;

KW gene therapy; NOV14b; prostatin precursor-like.
                                                                                                                           Human prostatin precursor-like NOV14b protein, SEQ ID NO:46.
                             ABB09524 standard; protein; 357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2001, 2001US-0260360P.
28-FEB2-2001, 2001US-027241TP.
02-MAX-2001, 2001US-0272817P.
05-UUL-2001, 2001US-0305660P.
12-UUL-2001, 2001US-0305660P.
10-SEP-2001, 2001US-0318405P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001; 2001US-0260018P.
08-JAN-2001; 2001US-0260360P.
28-FEB-2001; 2001US-0272411P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-2002; 2002WO-US000375.
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                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200253742-A2.
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04-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                               01-NOV-2002
                                                               ABB09524;
RESULT 1
               ABB09524
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Ellerman K, Malyankar U; Guo X, Shenoy S, Anderson D;

Guo X, Sh , Eisen A;

Sciore P, Elle ', Boldog F, Gu J, Miller CE, Edinger S, Scir M, Stone D, B I, Taupier RJ, 1 2002-583619/62 WPI; 2002-583619 N-PSDB; ABQ93902 Padigaru M, Rothenberg disorders. Gorman

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune

Claim 1c; Page 143; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14

(ABB09501-ABB09524), collectively referred to as NOVX proteins, and
nucleic acids encoding them (AB093879-AB093902). NOVX proteins, and
nucleotides are useful in the treatment, diagnosis or prevention of NOVXnucleotides are useful in the manufacture of a medicament for treating
ssociated disorders or in the manufacture of a medicament for treating
such disorders, with specific applications described for each of the 24
NOVX proteins, based on their homology to known proteins. Various
disorders are associated with NOVX proteins including neurological
disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
pain, behavioural disorders, addiction, tuberous sclerosis, cancers
ce gain, colorectal cancer, leukaemia and osteosarcoma), immune diseases
ce (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
ce yailous forms of arthritis, diabetes, thyroiditis, cardiovascular disease
ce (e.g., hypertension), reproductive disorders, enders, pancreatitis,
corrience, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
circhosis, glomerular endotheliosis, polycystic kidney disease, endocorriection communes of arthritish alprocessing-related disorders and disorders
circhosis, glomerular endotheliosis, polycystic kidney disease, endocorriection cathery regulation. NoVX nucleic acids and polypeptides may
competication of small molecules that modulate or inhibit processes such
characterogenesis, cell differentiation, cell montality, cellular
continence of priners or probes for forenesic byte and
compising NOVX nucleic acids are useful for producing non-human
continentifying and cloning NOVX homologues in other cell types. Cells
comprising NOVX nucleic acids are useful for studying the function and
comprising not contain and for incomplement and province and contained and cloning the desire the desired and contained and for incomplement and contained and for incomplement and contained and contained and contained and containe activity of NOVX proteins and for identifying and evaluating modulators of NOVX activity. The present sequence represents the prostatin precursor like protein NOV14b

Sequence 357 AA;

120 QVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGFLDGAHTR 120 180 180 240 240 300 9 09 GDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFP MAQKGVLGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW 121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD 121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD VQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ 181 VQEADPLPLPWVLQEVELKLIGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ 1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW QVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTR Gaps ., 0 100.0%; Score 1953; DB 5; Length 357; 100.0%; Pred. No. 5.2e-146; Indels . 0 Mismatches 0; Matches 357; Conservative Similarity 181 19 61 Query Match Local Db 엄 à q $\overset{\circ}{\circ}$ q δ ά δ

GDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYBAWIRBQVMGSEPGPAFF 300

d

Huntington's disease; Parkinson's disease; pain; Dehavioural disorder;

Huntington's disease; Parkinson's disease; pain; Dehavioural disorder;

M addiction, tuberous sclerosis; cancer; immune disorder; allergy;

KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

KW autoimmune disease; myasthenia gravis; asthma; alopedes;

KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;

KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

Atherosclerosis; cell signal processing-related disorder;

M metabolic pathway regulation disorder; cytostatic, neuroprotective;

M metabolic pathway regulation disorder; cytostatic, neuroprotective;

M metabolic pathway regulation disorder; prostatic, neuroprotective;

M defractological; antibacterial; antiatrhitic; hepatotropic; neurogenesis;

M differentiation; proliferation; molility; hematopoolesis; wound healing;

M angiogenesis; forensic biology; transgenic animal; drug screening;

W gene therapy; NOV14a; prostatin precursor-like; chromosome 16. The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and nucleotides are useful in the treatment, diagnosis to prevention of NOVX-associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24 Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune Ľ, 357 Γį 301 TQPQKTQSDCLHQTAFLDSARILLRPLSHISVGVSTGTKSLVLPWLSPHSLLGLWGF ä Tchernev VT, Liu X, Spytek KA; Lepley DM, Burgess CE, Vernet CAM, iore P, Ellermen K, Malyankar U; Boldog F, Guo X, Shenoy S, Anderson Human prostatin precursor-like NOV14a protein, SEQ ID NO:44. Human; NOVX; neurological disorder; Alzheimer's disease; Cherney Lepley DM, Burse, P. Ellerman K, Malywar, Shenoy S, Edinger S, Sciore P, Ell M, Stone D, Boldog F, G Taupier RJ, Miller CE, Claim 1c; Page 142; 323pp; English. Æ ABB09523 standard; protein; 344 08-JAN-2001; 20010S-0260360P.
28-FEB-2001; 20010S-0272411P.
02-VAR-2001; 20010S-0272417P.
05-UUL-2001; 2001US-030231P.
12-UUL-2001; 2001US-0305060P.
10-SEP-2001; 2001US-0318406P.
12-SEP-2001; 2001US-0318406P. 07-JAN-2002; 2002WO-US000375. 05-JAN-2001; 2001US-0260018P Grosse WM, (first entry) Alsobrook JP, (CURA-) CURAGEN CORP. 2002-583619/62. N-PSDB; ABQ93901 WO200253742-A2. Patturajan M, Rothenberg M, Padigaru M, T 01-NOV-2002 11-JUL-2002. Forman L, disorders. Kekuda R, ABB09523; RESULT 2 ABB09523 g ð

antibacterial; fungicide; gastrointestinal; antidiarrheic; laxative; haemostatic; anti-HIV; thrombolytic; anticoagulant; gynaecological; cardiovascular; antiarteriosclerotic; hypotemsive; vasotropic; antitheumatic; lamunosuppressive; antiallergic; antithyrointesive; antisthourit; thyromimetic; antiarthritic; uropathic; ophthalmological; antigout; thyromimetic; antiarthritic; uropathic; ophthalmological; antigout; thyromimetic; antiarthritic; uropathic; auditory; antisebornhaic; antidepressant; neuroleptic; antimfertility; antisebornhaic; crohn's disease; hypertension; autoimmune; inflammatory; anaemia; cell proliferative; developmental; epithelial; scabies; neurological; Alzheimer's disease; reproductive; ectopic pregnancy; gene therapy; vaccine; disorder; prostasin.

hepatotropic; osteopathic; antiemetic; antipyretic; virucide;

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disorders are associated with Novy proteins including neurological disorders are associated with Novy proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), caloredral cancer's, Heutengines including neurological cancers (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disease (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, incontinence, psoriasis, soleroderma, alopecia, ulcers, pancreatitis, incontinence, psoriasis, soleroderma, alopecia, ulcers, pancreatitis, cirrhosis, glomerular endothellosis, polycystic kidny disease, endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, contractions of identify cellular receptors or downstream effectors which the binds to a NOVX protein, and are also useful as targets for the identification of small molecules that modulate or inhibit processes such as neurogenesis, cell differentiation, cell motifility, cellular compisions on be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic bilds are useful as a source of primers or probes for forensic bilds comprising NOVX nucleic acids are useful for producing non-human transgenic animals which are useful for studying the function and activity of NOVX proteins and for identifying and cloning NOVX nucleic acids are useful for producing non-human cransgenic animals which are useful for studying the function and activity. The present sequence represents the prostatin precursor of NOVX activity. The present sequence represents the prostatin precursor of NOVX activity. The present sequence represents the prostatin processor.
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                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                               181 VQEADPLPLPWVLQEVELKLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ
                                                                                              1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW
                                                                                                                                          1 MAQKGVIGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW
                                                                                                                                                                                                                                                                                   121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD
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                                                                                                                                                                                        61 QVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTR
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                                                     Gaps
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    Length 344;
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                                              0; Indels
96.0%; Score 1874; DB 5; L
100.0%; Pred. No. 8.6e-140;
iive 0; Mismatches 0;
                                                Matches 344; Conservative
                          Local Similarity
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    Query Match
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Griffin JA, Swarnakar A; Au-Young J, Elliott VS; , Lu DAM, Lee EA; MG, Khan FA;

Baughn MR, Griff Gandhi AR, Au-3 ', Warren BA, Lu ane AM, Yao MG,

Azimzai Y, Kallick DA, Baughn Walia NK, Hafalia AJA, Gandhi L J. Thangavelu K, Lu Y, Warre ey CM, Arvizu C, Delegeane AM,

WPI; 2002-519664/55.

Sanjanwala MM;

Ramkumar J, Tribouley C

Yue H, Lal PG,

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N-PSDB; ABQ75956.

21-DEC-2000; 2000US-0257803P. 05-JAN-2001; 2001US-0260I10P. 19-JAN-2001; 2001US-026351P. 25-JAN-2001; 2001US-0264628P.

(INCY-) INCYTE GENOMICS INC.

05-DEC-2001; 2001WO-US046964. 08-DEC-2000; 2000US-0254399P.

WO200246383-A2.

13-JUN-2002

Homo sapiens

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The invention relates to an isolated Protein Modification and Maintenance (PMM) polypeptide. Polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMM. These include gastrointestinal disorders (e.g. Crohm's disease), cardiovascular disorders (e.g. unaemia), cell proliferative disorders, developmental disorders, epithelial disorders (e.g. scabies), neurological disorders (e.g. Alzheimer's disease) reproductive disorders (e.g. ectopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of protein modification and maintenance molecules. The found to have homology with rat prostasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
New isolated Protein Modification and Maintenance polypeptides, for diagnosis, and treatment of e.g. gastrointestinal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.1%; Score 1505; DB 5; Length 8 ilarity 100.0%; Pred. No. 3.2e-110; Conservative 0; Mismatches 0; Indels
                                                                                                                           Claim 1 (a); Page 174-176; 200pp; English
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Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 818 AA;
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8 8 8 8

anticonvulsant; neuroprotective; nootropic; cytostatic; antipsoriatic; antiasthmatic; dermatological; antidiabetic; antiparkinsonian; antianaemic; antiinflammatory; antiulcer; antianginal; cardiant;

Human; PMMM; protein modification and maintenance molecule;

Human PMMM Incyte ID 2751509CD1.

(first entry)

17-0CT-2002

ABB98135;

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ABB98135 standard; protein; 818

RESULT 3 ABB98135 157 157 217 217

97

Gaps

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Length 818; Indels 38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP

.77.1%; Score 1505; DB 5; I 100.0%; Pred. No. 3.2e-110; tive 0; Mismatches 0;

Query Match .77.1 Best Local Similarity 100. Matches 272; Conservative

38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWINGTLEP

98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP

98 AAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRIASPASLGPAVWP

VCL.PRASHRFVHGTACWATGWGDVQEADPL.PLPWVLQEVELRLIGEATCQCLYSQPGPFN LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT <u>irioilpemicagypegrruprogensegeruvceeggrwpgagirsfereggrrurpgvfr</u>

158 218 218 278

158

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AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309 AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309

VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLXSQPGPFN

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Human, protease, cancer; immune-related disorder; cardiovascular disease, neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
          VCLPRASHREVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN 217
                                             218 LTLQILPGMLCAGYPEGRRDTCQCBGGGFLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT
                                LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT
Sudarsanam S, Manning G, Caenepeel S;
                                                                                                                                                                                                                      of novel human protease #52
                                                                             AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                               278 AVATYEAWIREQVMGSEPGPAFFTQPQKTQSD 309
                                                                                                                                                         AAU82753 standard; protein; 818 AA
                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2000; 2000US-0214047P.
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                                                                                                                                                                                                                         Amino acid sequence
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N-PSDB; ABK31795
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                                                                             278
                                    218
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers anable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                               Kawai Y;
T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID NO 3347; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                             pai T, Hayashi K, Ishii S,
Nagai K, Kojima S, Otsuki
                                                                                                                                                       Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                       Human polypeptide, SEQ ID NO: 3347.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T,
                              AAM93568 standard; protein; 766
                                                                                                                                                                                                                                                                                                                                     L1-JAN-2000; 2000JP-00118774.
                                                                                                                                                                                                                                                                                      07-JUL-2000; 2000EP-00114089.
                                                                                                                                                                                                                                                                                                                    99JP-00194486
                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000; 2000JP-00183765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST
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                                                                                                                                                                                                                         EP1130094-A2.
                                                                                                                                                                                                                                                                                                                      08-JUL-1999;
                                                                                                                                                                                           Homo sapiens.
                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                         05-SEP-2001
                                                            AAM93568;
                AAM93568
RESULT
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The present invention relates to the isolation of novel human proteases, and the mucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. disorders, pain, sexual dysfunction, mood disorders, attention disorders, oppilition disorders, hypotension, pypertension, psychotic disorders, neurological disorders (e.g. Albeimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. thuman proteases of the invention

Sequence 818 AA;

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory

Claim 6; Fig 2R; 313pp; English.

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ABG04853;
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                                                  Kiao Y,
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                                                                          90 MINGTLEPAAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRIASPA 149
                                                                                                                     209
                                                                                                                                 61 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQRADPLPLPWVLQEVELRLLGEATCQCL 120
                                                                                                                                                           269
                                                                                                                                                                      renal failure, malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease.
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                                                                                                                                                                                                                                                                                                                                             Human, prostasin-like serine proteage, cytostatic, antiatherogclerotic, virucide, osteopathic, antiinflammatory, vasotropic, neuroprotective, trypsin-like, metastasis, autoimmune lesion, atherosclerosis;
                                                                                              1 MTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPA
                                                                                                                  150 SLGPAVMPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCL
                                                                                                                                                         210 YSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGR
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Serine protease trypsin family domain"
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162. .173
                                       Length 766;
                                                         Indels
                                                                                                                                                                                                             270 RNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Type I fibronectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Type I fibronectin domain"
                                     Query Match 61.5%; Score 1202; DB 4; Best Local Similarity 100.0%; Pred. No. 2.5e-86; Matches 220; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Apple protein domain"
.61. .174
                                                                                                                                                                                                                                                                                                                           Human prostasin-like serine protease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Trypsin_His region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Trypsin_ser region"
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                                                                                                                                                                                                                                                                  AAU75082 standard; protein; 178 AA.
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                                                                                                                                                                                                                                                                                                        (first entry)
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format directly from EPO
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                                   Query Match
Best Local Similarity
                   Sequence 766 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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This invention comprises the CDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease is useful fluid. An antibody specific for prostasin-like serine protease is useful for immunodetection and diagnosis of micro-metastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease (G.S. prion protein amyloid plaques of Genstmann-Straussler Syndrome, coreutzfeldt-Takob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease gene provides a therapeutic target of decreasing human prostasin-like serine protease cortivity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be useful to treat augment and inhibit the enzyme activity which may be useful to treat core record augment and inhibit the enzyme activity which may be useful to treat core record augment and inhibit the enzyme activity witch may be useful to treat core record augment and inhibit the human protease of human prostasin-like arriver and any prostasin-like serving arriver and any prostasin-like serving arriver and particularly debtal implants. Altered levels of human prostasin-like arriver and any contagned and the arriver, which the may be useful to treat contagned and inhibit the contagned and the protease and degradation of human prostasin-like arriver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human prostasin-like serine protease polypeptide and polymucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 IGADIALIRLASPASIGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 VELRILGEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELRIAGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #4844.
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23-JUN-2000; 2000US-0213588P.
20-MAR-2001; 2001US-0276909P.
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                                                                                                                                                                                                                                                                                                                              WPI; 2002-114576/15.
                                                                                                                                                                                                                                            Morozov V;
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                                                                                                                                     (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK13565
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRS) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 35212; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                     30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73
                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS69040.
                                                                                 WO200175067-A2.
                                          Homo sapiens.
                                                                                                                       11-OCT-2001
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153 PAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQ 212 61 PAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLIGEATCQCLYSQ 120 93 GTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLG GTLEPAAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLG Gaps -1 41.2%; Score 804.5; DB 4; Length 198; 96.2%; Pred. No. 1.3e-55; Indels PGPFNLTLQILPGMLCAGYPEGRRDTCQ-GDSGGPL 247 1; Mismatches 96.2%; Conservative Best Local Similarity Sequence 198 AA; Matches 150; 213 Query Match g ò g ð

152

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ABG96402 standard; protein; 343 AA. ABG96402; RESULT 8 ABG96402

PGPFNLTLQILPGMLCAGYPEGRRDTCQPSPEPGPM 156

121

(first entry) 11-DEC-2002 Human ovarian cancer marker OV80.

Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.

Homo sapiens.

WO200271928-A2.

19-SEP-2002.

14-MAR-2002; 2002WO-US007826

14-MAR-2001;

14-MAR-2001; 2001US-0276026P. 10-AUG-2001; 2001US-0311732P. 19-SEP-2001; 2001US-0323580P. 26-SEP-2001; 2001US-0324967P. 26-SEP-2001; 2001US-0325102P. 26-SEP-2001; 2001US-0325149P.

(MILL-) MILLENNIUM PHARM INC

Kovatis SG; Vieby PO, Kamatkar S, Gannavarapu M, Hoersch S, Kamatkan Morrisey MP, Olandt PJ, Sen A, Vie K, Schmandt RE, Zhao X, Glatt K; Morrisey MP, Oland u K, Schmandt RE, Lu K, Monahan JE, Meyers RE, Bast RC,

WPI; 2002-723277/78. N-PSDB; ABS76501. Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

Disclosure; Page 385; 481pp; English.

The present inversion relates to a new method involves comparing the expression level of a marker in a patient sample and the normal level of expression level of a marker in a control non-varian cancer sample, where the expression of the marker in a control non-varian cancer sample, where the marker is selected from 363 cancer markers described in the characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing cancer). The cancer markers may be used in the management and treatment cancer. The cancer as disease, or parkinson's disease, brain cancer. The cancer are disease, and the recurrence of ovarian cancer. The cancer markers may be used in the management and treatment cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningities of e.g. bacterial or viral meningities or encephalitis), inflammations (e.g. bacterial or viral meningities or encephalitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with the whether ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is labely to metastasize. selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the The present invention relates to a new method for assessing whether a

Sequence 343 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel method for determining if a human has, or is likely to develop, a malignant growth. The method comprises measuring the concentration of prostant as protein or mRNA, in a sample and comparing the result with one or more controls, where a level of prostatin expression that is significantly higher than in controls is indicative of cancer, or increased susceptibility. The assay is specifically used to detect ovarian cancer or a predisposition to it, but
                                                                                                                                                                                                                                                                                                   171 TGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG 230
                                                                                                                                   GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                                     GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                                                                                                                                                                                                         236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
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                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                           296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG---LLSPRLSEH 343
                                                                                        54 GOWPWOVSITYEGVHVCGGSLVSEOWVLSAAHCFPSEHHKE---AXEVKLGAHQLDSYSE
                                                                                                                                                                                                                                                                       TGWGDVQEADPLPLPWVLQEVELRLIGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR
                                                                                                                                                                                                                                                                                                                                                                         231 KDACÓGDSGGPLSCPVEGLWYLIGIVŚWGDACGARNRPGVYTLASSYASWIQSKV--TEL
                                                                 1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing cancer or susceptibility to it, useful particularly for ovarian cancer, comprises detecting increased levels of prostatin in blood or tissue.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostasin; human; malignant; cancer; ovarian cancer; breast cancer; prostate cancer; lung cancer; colon cancer.
                                 24;
 Length 343;
                                Indels
                                 129;
35.3%; Score 690; DB 5; 43.6%; Pred. No. 2.7e-46;
                                49; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 34-36; 36pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU78547 standard; protein; 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2000; 2000US-0231166P
              Best Local Similarity 43.6
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostasin protein
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N-PSDB; ABK12241
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostasin-like enzyme; human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; gene therapy; antisense therapy.
                                                                                                                                                                                                                                                                                                     GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                                                                                                                                                                                                   GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human prostasin-like enzyme polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLFLGLALG---LLSPWLSEH 343
may also be applicable to breast, prostatic, lung and colonic cancers. Using the method of the invention it was shown that in ovarian cancer, the highest levels of prostatin were found in stage II disease, suggesting that this marker is suitable for early detection. The presents expresents the human prostasin protein used in the method of invention as a marker for early detection of cancer or susceptability
                                                                                                                                                                                                                                                                  1 MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
                                                                                                                                                                                                                                                                                                                      54 GOWPWOVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                    TGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR
                                                                                                                                                                                                                                   1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                    24;
                                                                                                                                                                   Length 343;
                                                                                                                                                                ; Score 690; DB 5; Length 34; Pred. No. 2.7e-46; 49; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 343
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                                                                                                                                                                   35.3%;
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                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                   Similarity
                                                                                                                                   Sequence 343 AA;
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Best Local 9
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The invention comprises a method for assessing whether a patient is afflicted with breast cancer or ovarian cancer. The method involves the use of specific DAM markers. The method of the invention is useful in the detection and treatment of ovarian and breast cancer. Amino acid sequences ABJ37025 - ABJ37080 represent human breast/ovarian cancer-
                                                                                                                                                                                                                                                                                                                   Determining the presence of breast cancer in an individual, involves
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 193-194; 233pp; English.
                                                                                                                                                                                                                                                                                                                                          using specific polynucleotide markers.
                                                          21-JUN-2002; 2002WO-US019773.
                                                                                                 21-JUN-2001; 2001US-0300159P.
27-JUN-2001; 2001US-0301351P.
                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                      WPI; 2003-267848/26.
                                                                                                                                                                                                                                                                             N-PSDB; ABT31936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related proteins
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                  03-JAN-2003.
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                                                                                                                                                                                                           Veiby OP;
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                                                                      The invention relates to human prostasin-like enzyme polypeptides and methodology. The enzyme can be expressed by standard recombinant methodology. The polypeptide, polymucleotide and medulators are useful for treating diseases like metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), partheroselerosis, neurodegenerative disease and pathogenic infection, partheroselerosis, neurodegenerative disease and pathogenic infection, particularly viral infection. The prostasin-like enzyme gene provides a therapeutic target of decreasing the enzyme activity, in particular for treating or preventing metastatic cancer. Neurodegenerative diseases include for e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrapie. The agonists and anatagonists of the polypeptide may be useful to treat osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                      Paget's disease, degradation of bone implants particularly dental implants. Altered levels of human prostasin-like enzyme activity inhibit both smooth muscle cell proliferation and lipid accumulation and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                   the progression of restenciss and atherosclerosis. Anti-human prostasin-
like serine protease antibodies are useful for immunodetection and
diagnosis of micrometastases, autoimmune lesions and renal failure in
biopsy specimens, plasma samples and body fluids. The present sequence
represents the amino acid sequence of protein identified by Swiss Prot
Acon No. Q16651, used for comparison studies with the human prostasin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.3%; Score 690; DB 5; 43.6%; Pred. No. 2.7e-46;
                                      Disclosure; Fig 3; 125pp; English
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Matches 156; Conservative
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DAKVSTIKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG---LLSPWLSEH 343
                                                                                                                                                                                                                                                                                                                                                      54 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE
                                                                                                                                                                                                                                 1 MAOKGVLGPGOLGAVA----ILLIYLGILRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
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                                                                                 Gaps
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                 24;
       Length 343;
                                                                                 49; Mismatches 129; Indels
Query Match 35.3%; Score 690; DB 6; Best Local Similarity 43.6%; Pred. No. 2.7e-46; Matches 156; Conservative 49; Mismatches 129.
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or human polynucleotides or composition to more inversions a composition of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nagent that is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polynucleotides or method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that medulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chul) in an animal segmental nerve injury (Chul) in an animal segmental nerve injury (Shul) in an animal companied the sequence data for this patent did not form part of the printed the specification, but was obtained in electronic form directly from WIPO at the value of pain problemes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 DAKVSTLKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASPPNGLHCTV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 GOWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCRPSEHHKE---AYEVKLGAHQLDSYSE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 TGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a composition comprising two or more isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Gaps
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43.6%; Pred. No. 2.7e-46;
Live 49; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                       Costigan M;
                                                                                                                                                                                                                                                                                                                       Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp; English.
                                                                                                                                                                                   01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                              14-AUG-2002; 2002WO-US025765.
                                                                                                                                                           14-AUG-2001; 2001US-0312147P.
                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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Matches 156; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        GENBANK; 016651.
                     WO2003016475-A2
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The inversion in the control of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector identifying a nucleotide, a host cell comprising the vector to identifying a nucleotide sequence witch is differentially regulated in a naimal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypeptides or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic pain. The sequence presented is a human protein (shown in Table 2 of the readers or their any differentially expressed during pain. Note:
236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                      296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                289 QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG---LLSPWLSEH 343
                                       231 KDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKV--TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated
                                                                                                                                                                                                                                                                                                                                                                                                                        pain; neuronal tissue; gene therapy; segmental nerve injury; ccl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                Human Protein Q16651, SEQ ID NO 13257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                           ADD47561 standard; protein; 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page; 1017pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woolf C, D'urso D,
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                                                                                                                                                                                                                                                                                        ADD47561;
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                                                                                                                                                                                                                                                                                                                                                                                                     RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; NOV14a; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPIIFLPLFLFLGLALG---LLSPWLSEH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;
Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic;
Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                    GOWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE
                                                                                                                                                                                                                                                                                                                                                           TGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG
                                                                                                                                                                                    MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
                                                                                                                                                                                                                 GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD
                                                                                                                                                                                                                                                                          GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA
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                                                                                                                                                       --ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                        Gaps
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Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM;
                                                                                                                        24;
                                                                                          Length 343;
                                                                                        ; Score 690; DB 7; Length 34; Pred. No. 2.7e-46; 49; Mismatches 129; Indels
                                                                                                                                                     MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP--
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2001US-0260831P.
2001US-0272338P.
2001US-0274876P.
2001US-0284704P.
                                                                                          35.3%;
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                                                                                                                      156; Conservative
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                                                                                                      Local Similarity
                                                             Sequence 343 AA;
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28-FEB-2001;
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                                                                                           Query Match
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proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, Alba heart disease, inflammation, autoimmune IgA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NoV14a is a prostasin-like protein, and the NOV14a coding sequence localises to chromosome 16pl1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse, enzyme; transgenic; channel activating protease 1; CAP1; serine protease; seizure; epilepsy; therapeutic; agonist; anticonvulsant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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ΜM;
Κ,
                                                                                                                                 useful for prever
inflammation, or
tissue typing or
Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman IJ, Malyankar U, Millet I, Peyman J, Smithson G; Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.0%; Score 645; DB 5; Length 30
'41.3%; Pred. No. 8.5e-43;
ive 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channel activating proteage 1, (CAP1) protein.
                                                                                                                                 NOVX polypeptides and encoding polynucleotides, treating NOVX-associated disorders e.g. cancer, Alzheimer's disease, and in chromosome mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCF
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                                                                                                                                                                                                                      Claim 1; Page 98; 358pp; English.
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Matches 148; Conservative
                                                                                   2002-590674/63
                                                                                                                                                                                        pharmacogenomics.
                                                                                                     N-PSDB; ABN85392.
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 Taylor S, Tch
Alsobrook JP,
Macdougall J,
Gunther E, St
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PT Active-site 236..241

XX WO20283875-A2.

XX 24-OCT-2002.

XX 29-MAR-2001; 2001US-0280509P.

PR 08-AUG-2001; 2001US-021055P.

PR 29-MAR-2001; 2001US-021055P.

PR 29-MAR-2001; 2001US-021055P.

PR 29-MAR-2001; 2001US-021055P.

PR 29-MAR-2001; 2001US-021055P.

RW PL 2001 SE6186/05.

XX (DELT-) DELTAGEN INC.

XX Delta a pharmaceutical composition for treating epilepsy.

XX Props, ABS56430.

XX Propering a pharmaceutical composition for treating epilepsy.

XX The invention discloses a new transgenic mouse comprising a disruption in cranding there is no native expression of endogenous CAP1 gene. Transgenic compactibility to entire protease I (CAP1) gene. CAP1 is a serine protease and there is no native expression of endogenous CAP1 gene entibit an increased compactibility to enforce disruption in the CAP1 gene exhibit an increased succeptibility to selzures which are similar to epilepsy. Disclosed is a method for producing the transgenic mouse with a disruption in the CAP1 gene enchoded sequence homologous to at least a first or second polymolectide sequence homologous to at least a first or second polymolectide sequence homologous to at least a first or second correspendence of a ffecting a general protease. The transgenic compaction in a CAP1 gene method for producing the transgenic mouse with a mutation in a CAP1 gene (GAP1 a CAP1 agonist) as determining whether an agent modulates a CAP1 serine protease. The transgenic mouse, comprising a disruption in the CAP1 gene (GAP1 protein associated with a mutation in crashing contracting epilepsy. The sequence presenting a pharmaceutical composition for tracting epilepsy. The sequence presented is the mouse CAP1 protein and SCAP1 protein for protein and condition associated with a mutation for tracting epilepsy. The sequence presented is the mouse CAP1 protein for propagating a pharmaceutical composition for tracting epilepsy. The sequence presented is the mouse condition associated with a mutation in a CAP1 protein associated and a selectable manual and protease. The p
```

Query Match

32.1%; Score 627.5; DB 6; Length 339;
Best Local Similarity 41.4%; Pred. No. 2.3e-41;
Matches 144; Conservative 48; Mismatches 139; Indels 17; Gaps 9;
Qy 1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSG-PARG-PPSARIVGGSNAQPGT 57

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178 WGDVQEADPLPLPWVLQEVELRLLGEATCQCLXSQPGPFNLTLQILPGMLCAGYPEGRRD 237

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ga OX

8

Search completed: February 25, 2004, 15:46:53 Job time : 104 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 25, 2004, 15:37:18; Search time 45 Seconds (without alignments) 763.119 Million cell updates/sec Run on:

US-10-037-417-46 1953 1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	prostasin (EC 3.4.		tryptase (EC 3.4.2	$\overline{}$	enteropeptidase (E	tryptage (EC 3.4.2	EC 3.4	tryptase (EC 3.4.2	tryptase (EC 3.4.2	allik	tryptase (EC 3.4.2	tidas	tryptage (EC 3.4.2	hepsin (EC 3.4.21.	plasma kallikrein	mast cell tryptase		acrosin (EC 3.4.21	plasma kallikrein	enteropeptidase (E	acrosin (EC 3.4.21	acrosin (EC 3.4.21	~:	toma		acrosin (EC 3.4.21	(EC	(EC	
SUMMARIES	ΩI	A57014	JC7731	A32410	A38654	A56318	JC4171	S00845	A35863	B35863	KQHUP	A45754	A53663	C35863	S33777	KOMSPL	856160	A37344	S29599	KORTPL	A43090	JX0172	S47538	A47246	B32410	PLBO	A34170	S18407	A61545	B61545
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ن	Query Match	35.3	27.1	26.3	25.6	25.4	25.2	25.1	24.9	24.8	24.7	24.7	24.6	24.5	24.5	24.3	24.3	24.2	24.2	24.2	24.0	24.0	23.9	23.8	23.8	23.8	23.7	23.6	23.2	23.1
	Score	690	530	514.5	499	496	491.5	490.5	485.5	484.5	482.5	481.5	480	æ	478.5	475	474.5	473.5	473	47	469.5	469	467.5	465.5	₹#	464.5	462	٠	2	452
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low-density lipopr		plasmin (EC 3.4.21	coagulation factor	plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	coaqulation factor	plasmin (EC 3.4.21	serine proteinease	polyprotein - Afri	pancreatic elastas	pancreatic elastas	tryptase (EC 3.4.2	testicular serine	acrosin (EC 3.4.21
JE0315	S11674	PLPG	KFHU1	B30848	PLHU	PLMS	KFHU12	I46260	A47547	T30337	A26823	B26823	S68702	JE0105	A55283
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1113	421	790	625	810	810	812	615	810	786	1524	269	269	237	366	420
23.1	23.1	22.9	22.9	22.8	22.7	22.6	22.5	22.3	22.3	22.2	22.1	22.1	22.0	22.0	21.8
452	451	448	447.5	445.5	442.5	440.5	440	436	435	434.5	432.5	431	429.5	429.5	426
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A57014 Professin (EC 3. C.Species: Howo C,Date: 24-May-1 C,Accession: A57 R,Yu. Biol. Chem. 2 A,Atterence numb A,Accession: A57 A,Stetus: trans1 A,Molecule type: A,Residues: 1-34 A,Cross-reference B,Accession: A57 A,Residues: 1-34 A,Cross-reference B,Accession: A57 A,Residues: 1-34 A,Cross-reference B,Accession: A57 A,Residues: 45-6 C,Genetics: A,Residues: 45-6 A,Residues: 45-6 C,Genetics: A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-6 A,Residues: 45-	SULT 1 7014 7014 7014 7014 7014 7014 7014 701	54 GOWPWQVSITYEGVHVCGGS
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A;Residues: 1-276 (REZ> A;CES) NID:g200508; PIDN:AAA39988.1; PID:g200509
A;Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
A;Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
R;Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
A;Title: Different mouse mast call populations express various combinations of at least A;Reference number: A35646; MUID:90222202; PMID:2326280
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A;Residues: 1-276 <REY>
A;Residues: references: GBMS57625; NID:g200506; PIDN:AAA39987.1; PID:g200507
A;Croserreferences: GBMS57625; NID:g200506; PIDN:AAA39987.1; PID:g200507
A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37
S Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
                                                                                                                                                                                                                                                                                     structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A38654; B38654; B35646; I59478
R;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the CDNA and gene of mouse mast cell protease-6. Transcription 1
A;Reference number: A38654; MUID:91139682; PMID:1995638
                                                                                                                                                                                                                                                                                                                                                                                                                               %;Cross-references: GB:MZ4664; NID:g163982; PIDN:AAA30854.1; PID:g163983; GB:J02862
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase #status predicted <ACT>
F;31-275/Product: tryptase #status predicted <AMT>
F;31-276/Domain: trypsin homology <TRY>
F;31-276/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLRLLGEATCQCLYSQPGPFNLTLQILPG-----MLCAGYPEGRRDTCQGDSGGPLVC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVPIVENSMCDVQY-----HLGLSTGDGVRIVREDMLCAG--NSKSDSCQGDSGGPLVC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                         R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H. Biochemistry 28, 4148-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: A;Reference number: A32410; MUID:89352460; PMID:2504277
A;Accession: A32410
                                                                                                       tryptase (BC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LGSLVPVSPAP-----GQALQRVGIVGGREAPGSKWPWQVSLRLKGQYWRHICGGSLIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 SWVLSAAHCEMINGILEPAAEWSVIL---GVHSQDGPLDGAHTRAVAAIVVPANYSQVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GADLALIRIASPASLGPAVWPVCLPRASHRPVHGTACWATGWGDVQEADPLPPWVLQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 LYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGG---GHICGGSLIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.3%; Score 514.5; DB 2; Best Local Similarity .42.2%; Pred. No. 4.8e-33; Matches 124; Conservative 27; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-275 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecules 1-855 <KIS.
A;Cross-references: DDBJ:AB049189
A;Cross-references: DDBJ:AB049189
A;Experimental source: strain Male, 7-week-old
A;Satomi, S.; Yamasaki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001
A;Hitle: A role for membrane-type serine protease (MT-SP1) in intestinal epithelial turn
A;Reference number: JC7775; PMID:11573963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ).Comment: This erzyme, an epithelial-derived, type II integral membrane serine protease of specific proteins or peptides on the brushborder membranes. It also participates in lial migration and/or cell loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane-bound arginine-specific serine proteinase precursor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cibate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 03-Feb-2003
CiAccession: JC77731, JC7775
R;Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda,
R;Kishi, K.; Amazaki, 425-430, 2001
A;Title: Characterization of a membrane-bound arginine-specific serine protease from rat
A;Reference number: JC7731; MUID:21421307; PMID:11530019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 PWVLQEVELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL-V 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GGSLIAPSWVLSAAHCFMTNGTLEPA--AEWSVLLGVHSQD-GPLDGAHTRAVAAIVVPA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFNDFTFDYDIALLELEKPAEYSTVVRPICLPDNTHVFPAGKAIWVIGWGHTKEGGTGAL 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                          236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                  TGWGDVQBADPLPLPWVLQEVBLRLLGBATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR 235
                                                                                                                                                                                                                                                                                                       231 KDACÓGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRÞGVYTLASSYASWIQSKV--TEL 288
                                                                                                                                                                                                                                                                                                                                                                296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                      289 OPRVVPOTOESGPDSNLCGSHLAFSSAPAQGLIRPILFLFLFLGLAG---LLSPWLSEH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ARIVGGSNAQPGTWPWQVSLHH-GGGHIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: basolateral cell surface
C;Superfamily: membrane-bound arginine-specific serine proteinase
C;Keywords: protein digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.1%; Score 530; DB 2; Length 855; 39.9%; Pred. No. 1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYBAWIREQ 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: DDBJ:AB037898
C;Comment: This arm....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Contents: Small intestine
A;Accession: JC7775
A;Molecule type: mRNA
A;Residues: 1-855 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 112; Conserv
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                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics
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A,Map position: 21q21-21q21
C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell,
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Nyllernate names: mast cell tryptase
Nyllernate names: mast cell tryptase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4171
R;Ide, H.; Itch, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.;
J. Biochem: 118, 210-215, 1395
A;Title: cDNA sequencing and expression of rat mast cell tryptase.
A;Accession: JC4171
A;Molecule type: mRNA
A;Residues: 1-274 <IDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: DDBJ:D38455; NID:9556555; PIDN:BAA07486.1; PID:9556556 C;Comment: This enzyme is basically specific for a connective tissue mast ceinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||: ::||||||: |:||||| ::|| CGKKLAAQDITPKIVGSNAKEGAWPWVGLYYGGRLLCGASLVSSDWLVSAAHC-VYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | :: | : . | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 889 TDYIQPICLPEENQVFPPGRNCSIAGMGTVVYQGTTAN-----ILQEADVPLLSNERCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 TLEPAAEWSVLLGVHSQDGPLDGAHT--RAVAAIVVPANYSQVELGADLALLRLASPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPAVWPVCLPRASHRFVHGTACWATGWGDV----QEADPLPLPWVLQEVELRLIGEATCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGR----PEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNG
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or with amino-terminal myristoylation of the heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 496; DB 1; Length 101; Pred. No. 5.6e-31; 47; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F,825,876,971/Active site: His, Asp, Ser #status predicted
                                             C;Genetics:
A;Gene: GDB:PRSS7
A;Cross-references: GDB:384083; OMIM:226200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: trypsin; trypsin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GRRNRPGVFTAVATYEAWIR 287
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39.2%;
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            otated below)
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A)Cross-references: GB:U09860
C;Comment: The mechanism of association with the membrane of the intestinal brush border
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Kosidues: 1-1019 < KIT>
A; Cross-references: GB: 109860; NID: g746412; PIDN: AACS0138.1; PID: g746413
B; Kitamoto, Y:; Yuan, X:; Mu, Q:; McCourt, D.W:; Sadler, J.B.
B; Kitamoto, Y:; Yuan, X:; Mu, Q:; McCourt, D.W:
A; Kitamoto, Y:; Yuan, X:; Mu, Q:; McCourt, D.W:
A; Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compc
A; Reference number: A43090; MUID: 94329561; PMID: 8052624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the proteolyt
                                                                                                               R; Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson, Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and A;Reference number: I59478; MUID:94023807; PMID:8210998
A;Accession: I59478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 VGPHIKSPQLFRVQLREQYLYYGDQLLSLNRIVVHPHYYTRAEGGADVALLELEVPVNVST 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEPAAEWSVILGVHSQDGPL-DGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPSAR---IVGGSNAQPGTWPWQVSLHHGGG---HICGGSLIAPSWVLSAAHCFMTNGT
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                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-276 <RES>
A;Cross-references: GB:L31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ajdene: MMCP-6
AjIntrons: 24/1; 79/2; 168/1; 222/3
CjSuperfamily: trypsin; trypsin homology
CjSuperfamily: trypsin; trypsin proteinase; zymogen
CjKeywords: hydrolase; serine proteinase; zymogen
Fj1-21/Domain: signal sequence #status predicted <SIG>F;22-31/Domain: activation peptide #status predicted <ACT>F;22-31/Domain: activation peptide #status syedieted <ACT>F;32-268/Domain: trypsin homology <TRX>F;32-268/Domain: trypsin homology <TRX>F;75,122,225/Active site: His, Asp, Ser #status predicted
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C;Species: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change c;Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change C;Accession: B43090 R;Kitamoto, Y.; Veile, R.A.; Donis-Keller, H.; Sadler, J.B.
Biochemistry 34, 4562-4568, 1995
A;Title: cDNA sequence achromosomal localization of human entrance number: A56318; MUID:95234679; PMID:7718557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.6%; Score 499; DB 2; Length 276; 41.4%; Pred. No. 7.9e-32; Live 35; Mismatches 93; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enteropeptidase (EC 3.4.21.9) precursor [validated] N;Alternate names: enterokinase
                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: B43090
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 41.48
Matches 109; Conservative
                                                         A, Molecule type: protein A; Residues: 32-54 < RE3>
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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A; Introns: 21/1; 78/2; 177/1; 221/3
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A,Molecule type: protein
A,Residues: 31-38 <CRO>
A,Experimental source: pituitary
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A; Residues: 1-275 < VA2>
                                                                                                                                                                                                                                                                                                                                    A; Accession: A35863
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Biochemistry 27, 1067-1074, 1988
A; Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom
A; Reference number: S00845; MUID:88209431; PMID:2835076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 IPLTEYIQPVCLPAAGQALVDGKIĆTVTGWGNTQYYGQQAG-----VLQBARVPIISND 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 VCN-----GADFYGNQIKPKARPCAGYPEGGIDACQGDSGGPFVCEDSISRTPRWRLCGI 374
                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                        PAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLIGEATCQCLY-- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
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                                                                                                                                                                      47 IVGGSNAQPGTWPWQVSLHHGGG---HICGGSLIAPSWVLSAAHCFWINGTLEPAAEWSV 103
                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 ASLGPAVWPVCLPRASHRFVHGTACWATGWGDV----QEADPLPLPWVLQEVELRLLGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepsin (EC 3.4.21.-) - human
C.Species: Homo sapiens (man)
C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LSRWRVFAGAVAQASP----HGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 PAAEWSVILGVHSQDGPLDGAH--TRAVAAIVVPANY-----SQVELGADLALLRLASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYTGDDVPI-----VQDGMLCAG--NTRSDSCQGDSGGPLVCKVKGTWLQAGVVSWGEG
                                                                                                                                                                                                                                                                                                                                                                 --AVAAIVVPANYSQVELGADLALLRLASPASLG
                                                                                                                                                                                                                                                                                            75 -VGLHIKSPELFRVQLREQYLYYADQLLTVNRTVVHPHYYTVEDGADIALLELEIPVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                        ----SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFG
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A, Molecule type: mRNA
A, Residues: 1-417 <LEY>
A; Cross-treferences: EMBL: X07732; NID: G32063; PIDN: CAA30558.1; PID: g32064
C, Genetics:
A, Gene: GDB: HPN; TMPRSS1; hepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GDE:13685; OMIM:142440
A,Map position: 19411-19413.2
C,Superfamily: trypsin homology
C,Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: transmembrane #status predicted <TMN>
F;183-440/Domain: trypsin homology <TRY
F;188-204,201-359,322-338,349-381/Disulfide bonds: #status predicted
F;203,257,353/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                            43;
                      #status predicted (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 417;
                                                                             25.2%; Score 491.5; DB 2; Length 274; larity 40.2%; Pred. No. 3e-31; Conservative 20; Mismatches 87; Indels 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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F:30-266/Domain: trypsin homology <TRY>
F:73,120,223/Active site: His, Asp, Ser #status p:
F:131/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAEANRPGIYTRVTYYLDWIHRYV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                                                                                                                                                                           104 LLGVHSQDGPLDGAHTR
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Matches 111; Conserv
                                                                                      Query Match
Best Local Similarity
Matches 106; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               tryptase (EC 3.4.21.59) I precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 1.2-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000 C;Accession: A55863; D35863; A60939; A39326 R;Vanderslice, P.; Ballinger, S.M.; Tam, B.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. R;Vanderslice, P.; Ballinger, S.M.; Tam, B.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. A;Title: Human mast cell tryptase: multiple connas and genes reveal a multigene serine pr A;Reference number: A35863; MUID:90251647; PMID:2187193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Residues: 1-275 <VAN>
A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
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R;Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, J. Leukoc. Biol. 47, 409-419, 1990
A;Title: Purification of tryptase from a human mast cell line.
A;Reference number: A60939; MUID:90244210; PMID:2110591
A;Accession: A60939
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261 TSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQ 302
                                                                 C, Superfamily: trypsin, trypsin homology
C, Keywords: hydrolase; serina proteinase; zymogen
C, Keywords: hydrolase; serina proteinase; zymogen
F,12.1)Domain: signal sequence #status predicted <ACI>F,22.30/Domain: activation peptide #status predicted <ACI>F,31.275/Product: tryptase I #status experimental <AMI>F;31.26/Thomain: tryptase I #status experimental <AMI>F;31.26/Thomain: trypsin homology <TRY>F;31.224/Active site: His, Asp, Ser #status predicted
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A;Cross-references: GDB:127575; OMIM:229000
A;Boross-references: GDB:127575; OMIM:229000
A;Boross-references: GDB:127575; OMIM:229000
A;Boross-references: GDB:127575; OMIM:229000
A;Boross-references: GDB:127575; OMIM:229000
C;Boross-references: GDB:127575; OMIM:229000
C;Boross-references: GDB:127575; OMIM:229000
F;1-19/Domain: signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status predicted <MAT>F;1-19/Domain: sple repeat <AP1>F;10-199/Domain: apple repeat <AP2>F;20-109/Domain: apple repeat <AP2>F;20-289/Domain: apple repeat <AP3>F;20-289/Domain: apple repeat <AP4>F;20-289/Domain: apple repeat <AP4>F;20-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-284/SIG-2
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A; Molecule type: protein
A; Molecule type: protein
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A; Molecule type: 20-27; Molecule type: 20-27; Molecule type: 20-27; Molecule type: 20-27; Molecule type: 20-27; Molecule type: 20-27; Molecule type: 20-27; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22; Molecule type: 21-22;
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R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemiatry 30, 2050-2056; 1991
A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of A;Reference number: A37939; MUID:91152016; PMID:1998666
                                                                                                                                                                                          NyAlternate names: kininogenin; plasma prekallikrein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: A00921; A37939
R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
B;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
A;Chung, D.W.; Pujikawa, K.; McMullen, B.A.; Davie, E.W.
A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four A;Reference number: A00921; MuID:86243359; PMID:3521732
A;Accession: A00921;
A;Accession: A00921;
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40.2%; Pred. No. 3.9e-30;
tive 33; Mismatches 97;
                                                                                                                                                plasma kallikrein (EC 3.4.21.34) precursor - human
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A; Residues: 1-638 <CHU>
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Cispecies: Home sapiens (man)
Cibate: 03.7-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
Cibate: 03-Reb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
Cibatession: B35863; A37123; I59473
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Roco. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple coRNs and genes reveal a multigene serine px
A;Reference number: A35863; MUID:90251647; PMID:2187193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA; DNA
A,Residues: 1-275 < vANA.
A,Cross-references: GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983
A,Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic
R;Miller: J.S.; Moxley, G.; Schwartz, L.B.
K;Miller: Noxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870; 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: mRNA
A, Residues: 1.275 <mil.2
A, Cross-references: GB: M3748B; NID:g179583; PIDN:AA51843.1; PID:g179584
A; Cross-references: GB: M3748B; NID:g179583; PIDN:AA51843.1; PID:g179584
R; Blom, T.; Hellman, L.
Scand. 7. Immunol. 37, 203-208, 1993
Scand. 7. Immunol. 37, 203-208, 1993
A; Title: Characterization of a tryptase mRNA expressed in the human basophil cell line
A; Reference number: I59473; MUID:93166209; PMID:8434231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDAKYHLGAYTGDDVRİVRDDMLCAG--NTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCLYSOPGPFNLTLQIL-PGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 ASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQBVELRLLGEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLH-HG--GGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-275 <RES>
A;Cross-references: GB:S5551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A;Experimental source: basophil cell line KU812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.8%; Score 484.5; DB 2; Length 275; 41.7%; Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Keywords: hydrolase; serine proteinase; zymogen
;1-21/Domain: signal sequence #starus predicted <SIG>
;22-30/Domain: activation peptide #starus predicted <ACT>
;31-275/Product: tryptase I #starus predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A37193; MUID: 90369005; PMID: 2203827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGCGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 EGCAOPNRPGIYTRVTYYLDWIHHYV 271
                                                                                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) II precursor - human
EGCAQPNRPGIYTRVTYYLDWIHHYV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:125890; OMIM:191080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: tryptase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 41.73
Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: B35863
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qq à q à d

RESULT 11

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A; Packrichian: cleaves activation peptide from trypsinogen to produce active trypsin A; Pathway: intestinal digestive hydrolase cascade
A; Pathway: intestinal digestive hydrolase cascade
C; Superfamily: enteropeptidase; CIr/CIs repeat homology; LDL receptor ligand-binding rep
C; Superfamily: enteropeptidase; serine proteinase; transmembrane protein; zymogen
C; Scywords: alycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F; 22-117/Product: enteropeptidase mini chain #status predicted «MCH»
F; 118-799/Product: enteropeptidase heavy chain #status predicted «HCH»
F; 119-236/Domain: LDL receptor ligand-binding repeat homology «LDLL»
F; 5357-519/Domain: CIr/CIs repeat homology «CIR»
F; 541-646/Domain: CIr/CIs repeat homology «CIR»
F; 568-692/Domain: LDL receptor ligand-binding repeat homology *LDLL2»
F; 693-798/Domain: LDL receptor cysteine-rich domain homology #status atypical «SRC F; 693-798/Domain: trypsin homology «CIR»
F; 690-1034/Product: enteropeptidase light chain #status predicted «LCH»
F; 116-147, 170, 194, 283, 343, 350, 403, 455, 485, 518, 549, 645, 697, 701, 721, 740, 761, 804, 863, 902, 96
F; 787-911, 825-841, 925-992, 956-971, 982-1010/Disulfide bonds: #status predicted
F; 840, 891, 986/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ri,
A;Cross-references: GB:D30799; NID:g505122; PIDN:BAA06459.1; PID:g505123
A;Note: parts of this sequence, including the amino ends of three chains isolated from t c;Comment: The mechanism of association with the membrane of the intestinal brush border otated below) or with amino-terminal myristoylation of the heavy chain.

C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light) ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #text_change 07-Mar-2003
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Mar-2003
C;Accession: C35863; B35863; A38893
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A;Reference number: A35863; MUID:90251647; PMID:2187193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          958 ÇÜMPEYNIT----ENMMCAĞYERĞGIDSCÇĞDSĞĞPLMCLENNRWILLAĞVISFGYÇÇALP 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 CGR----PEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 TLEPAAEWSVILGVHSQDGPLDGAH - TRAVAAIVVPANYSQVELGADLALLRLASPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  846 NLEP-SKWRAILGLHMTSN-LTSPQIVTRLIDBIVINPHYNRRRKDSDIAMMHLEFKVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GPAVWPVCLPRASHRFVHGTACWATGWGDV-QEADPLPLPWVLQEVELRLLGEATCQCLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   904 TDYIQPICLFPENQVFPPGRICSIAGWGKVIYQGSPAD---ILQRADVPLLSNEKCQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 480; DB 1; Length 10.
38.5%; Pred. No. 1e-29;
Live 46; Mismatches 92; Indels
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C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014 NRPGVYARVPKFTEWIQ 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to GenBank, April 1990
A;Reference number: A38893
A;Accession: A38893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 9-275 < VAN>
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A; Molecule type: DNA
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A; Residues: 1-274 < MIL)
A; Rolecule type: mRNA
A; Residues: 1-274 < MIL)
A; Rolecule type: mRNA
A; Roceas: 1-274 < MIL)
A; Clin. Invest. 86, 864-870, 1990
J. Clin. Invest. 86, 864-870, 1990
A; Title: Cloning and characterization of a second complementary DNA for human tryptase.
A; Reference number: A37193; MUD: 90369005; PMID: 2203827
A; Reference number: A37193; MUD: 90369005; PMID: 2203827
A; Residues: 1-274 < MIZ>
A; Roceasion: B37193
A; Molecule type: mRNA
A; Residues: 1-274 < MIZ>
A; Cross-references: GB: M30038
A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Prd
C; Superfamily: trypsin, trypsin homology
C; Reywords: hydrolase; serine proteinase; zymogen
F; 1-21/Domain: activation peptide #status predicted < ACT>
F; 22-30/Domain: activation peptide #status predicted < ACT>
F; 31-266/Domain: trypsin homology < TRY>
F; 31-266/Domain: trypsin homology < TRY>
F; 74,120,223/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 -- LGPDVKDLATLRVNS-----GTHLYYQDQLLPVSRIMVHPQFYIIQTGADIALLELE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 SPASIGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                  C,Date: 03-Unn-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997 C,Accession: A45754, B37193 R;Miller, J.S.; Westin, E.H.; Schwartz, L.B. J.C.in, Invest. 84, 1188-1195, 1989 A;Title: Cloning and characterization of complementary DNA for human tryptase. A,Reference number: A45754, MUID:90009311; PMID:2677049 A;Accession: A45754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enteropeptidase (BC 3.4.21.9) precursor [validated] - pig
NyAlternate names: enterokinase
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: O7-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
Cispecies: O7-Oct-1994 Esquence_revision 09-Aug-1996 #text_change 28-Apr-2003
Cispecies: O7-Oct-1994 Esquence_revision 09-Aug-1996 #text_change 28-Apr-2003
Cispecies: A53663
Nithie: Structural characterization of porcine enteropeptidase.
A;Thile: Structural characterization of porcine enteropeptidase.
A;Thile: Structural characterization of porcine enteropeptidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 GCGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAQPNRPGIYTRVTYYLDWIHHYV 270
                                                                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) alpha precursor C; Species: Homo sapiens (man)
                                                            611 YTKVAEYMDWILEKTQSSD
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Query Match Matches

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completed: February 25, 2004, 15:50:30
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A; Molecule type: mRNA
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Biochim. Biophys. Acta 1173, 350-352, 1993
A;Title: Cloning and sequence analysis of rat hepsin, a cell surface serine proteinase.
A;Reference number: S33777; MUID:93305733; PMID:8318546
A;Accession: S33777
A;Status: preliminary
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQRADPLPLPWVLQEVELRLLGEAT 205
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                                                                                                                                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: S33777; S32013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| : | ||||| :: | ||||||| : | :||||||| CGRRKLPVDRIVGGDDSSLGRWPWQVSLRYDGTHLCGGSLLSGDWVLTAAHCFPERNRV-
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                                                                                                                                                                                                                                                                                                                                                                                             FMINGILEPAAEWSVLL---GVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRL
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                                                                                                                                                                                                                                                                                                         32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLH---HGGGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                    AYAAPAPGQALQRVGIVGGQBAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHC
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A, Residues: 9-131, 'K', 132-275 < VA3>
A, Cross-references: GB: M33493; NID: g339984; PIDN: AAA36780.1; PID: g339985
C, Superfamily: trypsin, trypsin homology
C, Superfamily: trypsin, trypsin homology
C, Keywords: hydrolase; serine proteinase, zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>F;2-30/Domain: activation peptide #status predicted <ACT>F;2-30/Domain: trypsin homology <TRY>F;31-267/Domain: trypsin homology <TRY>F;31-267/Domain: trypsin homology <TRY>F;74,121,224/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 PAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQV---
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                                                                                                                                                                                                                       24.5%; Score 478.5; DB 2
41.0%; Pred. No. 3.2e-30;
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                                                                                                                                                                                                                                                                  109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepsin (EC 3.4.21.-) - rat
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Matches 107; Conserv
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                                                                                                                                                                                                                                             Similarity
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Best Local S
Matches 109
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A; Molecule Type: mkma
A; Molecule Type: mkma
A; Molecule Type: mkma
A; Molecule Type: mkma
A; Residues: 1-638 cSEL>
A; Cross-references: GB:M58588; NID:g200358; PIDN:AAA63393.1; PID:g200359
A; Cross-references: GB:M58588; NID:g200358; PIDN:AAA63393.1; PID:g200359
A; Note: part of this sequence, including the amino ends of both the heavy and light chair c; Comment: This protein, synthesized in the liver, circulates as a noncovalent complex wi c; Comment: This protein, sortivated by factor XIIa, which cleaves the molecule into a light are linked by one or more disulfide bonds.
C; Superfamily: coaqulation factor XI; trypsin howlogy
C; Keywords: blood coaqulation; diplication; fibrinolysis; glycoprotein; hydrolase; inflam C; Momain: signal sequence #status predicted <SIG>
F; 20-109/Domain: apple repeat cAP1>
F; 20-109/Domain: apple repeat cAP2>
F; 20-109/Domain: apple repeat cAP2>
F; 20-109/Domain: apple repeat cAP4>
F; 20-109/Domain: apple repeat cAP4>
F; 20-109/Domain: apple repeat cAP4>
F; 20-109/Domain: apple repeat cAP4>
F; 20-109/Domain: apple repeat cAP4>
F; 21-104, 47-7, 51-57, 111-194, 137-166, 141-147, 201-284, 227-256, 231-237, 292-375, 318-347, 322-77, 21-2, 308, 396, 494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 434, 483, 578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasma kallikrein (EC 3.4.21.34) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A36557
R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont
DNA Cell Biol. 9, 737-748, 1990
A;Fitle: Mouse plasma kallikrein: cDNA structure, enzyme characterization, and comparison
A;Reference number: A36557; MUID:91090844; PMID:2264928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535 LOKATIPLVPNEECOKKYRD------YVINKOMICAGYKEGGTDACKGDSGGPLVCKHS 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQEVELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCREG 252
211 SOPGPFNLTLOILPGMLCAGYPEGRRDTCQGDSGGPLVCEE----GGRWFQAGITSFGFG 266
                                                                       ---spdfygnolkprmfcagypEdgldacogbsedhfycEdrisgrshmrlcGlvswGr6 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 VSEGNYDIALIKLQTPLNYTEFQKPICLPSKADTNTIYTNCWVIGWGYTKEQGETQN--I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 SDSYS--LYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLH---HGGGHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 SSGYSLRLCKLVDS-----PDC-TTKINARIVGGTNASLGEWPWQVSLQVKLVSQTHLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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                                                                                                                                                                                                                                                      CALARKPGVYTKVIDFREWIFQAIKTHSEATGMVTQP 416
                                                                                                                                                                          CGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQP 303
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 25, 2004, 14:37:37; Search time 49 Seconds (without alignments) 379.368 Million cell updates/sec

US-10-037-417-46 1953 1 MAQKGVLGPCQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 regidues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q16651 homo sapien	นรถแ	rattu	РОШО	Ogingo bomo sapien	рошоц	рошо	Q9y6m0 homo sapien	mus	gnw	Q9qul7 mus musculu	Enm	mus m		Q9xsm2 ovis aries	ane	mus r	рошо	рошо	Q8k1t0 mus musculu		P05981 homo sapien		homo	homo	homod	74 sus £	P15157 homo sapien	11 rattı	Q9h3s3 homo sapien	P26262 mus musculu	P50342 meriones un
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SUMMARIES		HUMAN	MOUSE	PSS8_RAT	HUMAN	TMS6 HIMAN	HUMAN	ST14 HUMAN	TEST HUMAN	TMS6_MOUSE	TEST_MOUSE	TRYG MOUSE	MOUSE	BSS4 MOUSE	TRYT CANFA	SHEEP	TRYT PIG	OUSE	UMAN	OMAN	TMS3_MOUSE	MCT6_RAT	UMAN	HEPS MOUSE	TRB1 HUMAN	TRB2 HUMAN	HUMAN	PIG	HUMAN	AT	HUMAN	MOUSE	TRYT MERUN
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P14272 rattus norv Q9y5q5 homo sapien	P98072 bos taurus. P23578 mus musculu	P48038 oryctolagus	Q02844 mus musculu	P19236 canis famil	P06868 bos taurus	P08001 sus scrofa	P29293 rattus norv	P27435 rattus norv	Q9er04 mus musculu
KAL RAT CORI HUMAN	ENTK_BOVIN ACRO_MOUSE	ACRO_RABIT	MCT7 MOUSE	TRYM CANFA	PLMN BOVIN	ACRO_PIG	ACRO_RAT	MCT7 RAT	TMS5_MOUSE
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473	469.5	467.5	465.5	464.5	464.5	462	460.5	459	458.5
3.5 3.5	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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MEROPS; S01.158; -. MGD; MGD; MGI:1923810; Prss8.
                                                                                                                                                                        STANDARD;
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32
44
322
                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                        PSSB MOUSE
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 GOWPWOVSIIYEGVHVVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE
                                    kidney, lung, pancreas, colon, bronchus and renal proximal tubular cells. In the prostate gland it may be synthesized in epithelial cells, secreted into the ducts, and excreted into the seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTWPWOVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps
  SUBCELLILAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS.
                              TISSUE SPECIFICITY: Found in prostate, liver, salivary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (POTENTIAL) 98DD6447F5A8C1B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                  MAIN; 60:0053; C:extracellular space; TAS. GO; GO:000586; C:plasma membrane; TAS. GO; GO:0008236; C:plasma membrane; TAS. GO; GO:0008236; F:serine-type peptidase activity; TAS. InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.

Pfam; PF00089; trypsin; 1.

RRINTS; PR00122; CHYMOTRYBSIN.

SMART; SM00020; Tryp_SPC; 1.

RROSITE; PS0240; TRYPSIN DOM; 1.

RROSITE; PS00135; TRYPSIN HIS; 1.

RROSITE; PS00135; TRYPSIN_SRE; 1.
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CHARGE RELAY SYSTEM.
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ACTIVATION PEPTIDE.
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.3%; Score 690; DB 1; 43.6%; Pred. No. 1.1e-47;
                                                                                    SIMILARITY: Belongs to peptidase family S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
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                                                                                                                                                                                                                     EMBL; BC001462; AAH01462.1; -.
                                                                                                                                                                                               EMBL; L41351; AAC41759.1; -.
EMBL; U33446; AAB19071.1; -.
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MEROPS; S01.159; -.
Genew; HGNC:9491; PRSSB.
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disulfide bond.
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TGWGDVQEADPLPLPWVLQEVELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR 235
                                                                                                                                                                                                231 KDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKV--TEL 288
                                                                 171 TGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG 230
                                                                                                                                      236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                        296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                             289 QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLIRPILFLPLGLALG---LLSFWLSEH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIANE-20235202; PubMed=10770960; Vuagniaux G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N., Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.; "Activation of the amiloride-sensitive epithelial sodium channel by the serine protease mCAP1 expressed in a mouse cortical collecting duct cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostasin precursor (EC 3.4.21.-) (Channel activating protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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ACTIVATION PEPTIDE (BY SIMILARITY).
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 AA
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Interpro; IPR001254; Peptidase_S1.
Interpro; IPR001314; Peptidase_S1A.
Fram; PF001099; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SF0; 1.
PROSITE; PS00130; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN JSF1.
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HSSP; P00734; 1UVS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 WPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE---AYEVKLGAHQLDSYSNDT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYBAWIREQVMGSEPGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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SIMILARITY).
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                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  32.3%; Score 631; DB 1; Length 342; 41.4%; Pred. No. 5.2e-43; ive 48; Mismatches 139; Indels :
BY SIMILARITY.
POTENTIAL.
SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYST
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Adachi M., Kitamura K., Miyoshi T., Tomita K.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                  0620DE88ED187D0F CRC64;
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
26-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     36729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 146; Conservative
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ID _PSS8_RAT
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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f SIMILARITY).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.7%; Score 620; DB 1; Length 34 40.8%; Pred. No. 3.9e-42; ive 50; Mismatches 139; Indels
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A -> V (IN REF. 1).
SIMILARITY: Belongs to peptidase family Sl
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                                                                                                                                 EMBL, AF202075; AM32641.1; -...
HSSP: P00734; 1UVS.
HIGEPPO: IPR009003; Cyg_Ser_trypsin.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR00134; Peptidase_S1A.
PERM: PR00089; trypsin.; 1.
PRNYS; PR00722; CHYMOTRYPSIN.
SMART; SM00000; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_LDM; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                      POTENTIAL.
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321 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mittman S., Agnew W.S.;
"Organization and alternative splicing of CACNAIH.";
"Organization and alternative splicing of CACNAIH.";
"Organization and alternative BMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Membrane-anchored (Potential).
-!- TISSUB SPECIFICITY: Expressed in many tissues.
-!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which differ by 5 residues.
-!- SIMILARITY: Belongs to peptidase family SI. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99452974; PubMed=10521469; MEDLINE=99452974; PubMed=10521469; Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C., Priend D.S., Krilis S.A., Stevens R.L.; "Identification of a new member of the tryptase family of mouse and human mast cell proteases which possesses a novel COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                           "Characterization of human gamma-tryptases, novel members of the chromosome 16p mast cell tryptase and prostasin gene families."; J. Immunol. 164:6566-6575(2000).
                                                                                                                                                                                                                                                                                                       MEDLINE=20302813; PubMed=10843716;
Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M.,
Wolters P.J., Verghese G.M.;
                                                                                                                                             (Transmembrane tryptase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew, HGNC:14114, TPSG1.

InterPro; IPR00903; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

Interpro; IPR001254; Peptidase_S1A.

Pfam; PF00089; trypsin; 1.

PRINTS; PR0772; CHYMOTRYPSIN.

PROSITE; PS0124; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; FALSE NEG.

Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRYPTASE GAMMA LIGHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2)
                    OSTREAM STANDARD; PRT; 321 AA.

QSNRRZ; Q9C015; Q9NRQB; Q9UBB2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
17-OCT-2001 (Rel. 40, Last snucration update)
17-YPGASE gamma precursor (EC 3.4.21.-) (Transmitted)
17-OCT CONTRACTOR (TRANSMITTER)
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17-OCT CONTRACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydrophobic extension.";
J. Biol. Chem. 274:30784-30793(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF191031; AAF76457.1; -.
EMBL; AF195508; AAF76458.1; -.
EMBL; AF175759; AAF03697.1; -.
EMBL; AF17552; AAF03695.1; -.
EMBL; AF22563; AAF03695.1; -.
HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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          RESULT 4
TRYG_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRIRRMHVCGGSLLSPQWVLTAAHCF--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GILEPAAEWSVLLGVHSQDGPLD---GAHTRAVAAIVVPANYS-QVELGADLALLRLASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 ASLGPAVWPYCLPPASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 LYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Pancreasin preursor (EC 3.4.21.-) (Marapsin) (Channel-activating protease 2) (CAPH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22439795, PubMed-12441343,
Bhagwandin V.J., Hau L.W.-T., Mallen-St Clair J., Wolters P.J.,
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.8%; Score 582; DB 1; Length 321; 46.0%; Pred. No. 3.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.; "Cloning, sequencing and expression of marapsin, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Okaze H., Hayashi A., Kozuma S., Saito T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                    /FTIG=VAR 012097.

| -> M (IN GAMMA-II).

| FTIG=VAR 012098.

| FTIG=VAR 012099.

| FTIG=VAR 01209.

| -> I (IN GAMMA-II).

| FTIG=VAR 012100.

| -> F (IN GAMMA-II).

| FTIG=VAR 012101.

| FTIG=VAR 012101.

| FTIG=VAR 012101.

| FTIG=VAR 012101.
                    INTERCHAIN (POTENTIAL).
BY SIMILARITY.
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BY SIMILARITY.
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BY SIMILARITY.
A SIMILARITY.
A SIMILARITY.
M -> V (IN GAMMA-II).
/FIId=uvar_012097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 RPNRPGVYTRVPAYVNWIRRHITASGGSESG--YPRLP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         33827 MW;
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 NGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPAN--YSQVELGADLALLRLASPA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPWVLQBVELRLLGBATCQCL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 YSQPGPFNLTLQILPG-MLCAGYPEGRRDTCQGDSGGPLVCBEGGRWFQAGITSFGFGCG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AKAATACGRPRMINRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCF-- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWT 91
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                      "Structure and activity of human pancreasin, a novel tryptic serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLARACE .....
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
(TYTOWNAC. ..) (POTENTIAL).
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SIMILARITY)
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42.2%; Pred. No. 1.1e-37;
tive 32; Mismatches 114; Indels 14;
                                            peptidase expressed primarily by the pancreas.";
J. Biol. Chem. 278:3363-3371(2003).
-!- SIBCLELBULAR LOCATION: Secreted.
-!- TISSUE SCIFICITY: Expressed predominantly in the pancreas.
-!- PTM: N-91ycosylated.
-!- FTM: N-91ycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.
SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LINKED (GLCNAC. . .) (PC 67BDC93EC70BFF7B CRC64;
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(BY
(BY
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PANCREASIN.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (CHARGE RELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Fram; PF000089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SF0; 1.
PROSITE; PS00130; TRYPSIN LDM; IPROSITE; PS00135; TRYPSIN LIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AJ306593; CAC35467.1; -. EMBL; AB056161; BAB85497.1; -. EMBL; AY030095; AAK38168.1; -. HSSP; P00734; 1UVS. MEROPS; SO1.074; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31940 MW;
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Parage C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Nadern E.J., Lu X., Gibbs R.A., Mring M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blacelley R.W., Touchman U.W., Greme E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=22241917; PubMed=12149247;
Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.;
"Matriptase-2, a membrane-bound mosaic serine proteinase predominantly expressed in human liver and showing degrading activity against extracellular matrix proteins.";
J. Biol. Chem. 277:37637-37646(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22668120; PubMed=12784999;
Netzel-Arnett S., Hooper J.D., Szabo R., Madison E.L., Quigley J.P.,
Bugge T.H., Antalis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Membrane anchored serine proteases: a rapidly expanding group of surface proteolytic enzymes with potential roles in cancer.";

Cancer Metastasis Rev. 22:237-258(2003).

-!- FUNCTION: May play a specialized role in matrix remodeling processes in liver.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 9-811 FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOCIA=QBIUB0-2; Sequence=VSP_008379, VSP_008380;
Note=No experimental confirmation available;
-:- TISSUE SPECIFICITY: Liver specific.
-:- SIMILARITY: Delongs to peptidase family S1.
-:- SIMILARITY: Contains 2 CUB domains.
-:- SIMILARITY: Contains 3 LDL-receptor class A domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=Q8IU80-1; Sequence=Displayed;
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InterPro; IPR000103; Cys_Ser_trypsin.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR001124; Peptidase_SI.
InterPro; IPR001314; Peptidase_SI.
Pfam; PF00431; CUB; I.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY055384; AAL16414.1; --
EMBL; AL022314; -; NOT ANNOTATED_CDS.
EMBL; BC039082; AAH39082.1; --
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00192; LDLA; 3.
SMART; SM00020; TTYP_SPC; 1.
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PROSITE; PS01180; CUB; 1.
PROSITE; PS01209; LDLRA 1; 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane; Glycoprotein; Alternative splicing.
CYTOPLASMIC (POTENTIAL).

CATOPLASMIC (POTENTIAL).

CATOPLASMIC (POTENTIAL).

CATOPLASMIC (TYPE-II MEMBRANE PROTEIN)
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Q9GZM4; 043342;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
18-ABRAIN-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)
PRSS22 OR PRSS26 OR BSSP4.
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/FTId=VSP 008380.
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
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PROSITE; PS00134;

sapiens (Human)

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A MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B chapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.B., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubzarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzzy D.W., Sodergren E.J., Lu X., Gibbs R.A.,

A Hakesley R.W., Touchman J.W., Garcia A.M., Gabs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rabacsley R.W., Touchman J.W., Grammar M.R.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Scheni J.E., Jones S.J.M., Marra M.A.;

Runn and mouse cDNA sequences ";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16503(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wong G.W., Stevens R.L.; "Identification of a new member of the chromosome 16 family of serine
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                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                           Mitsui S., Okui A., Kominami K., Yamaguchi N.; "Cloning and characterization of a human brain-specific serine protease, hBSSP-4.";
                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam, Pr00089; trypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB010779; BAB20263.1; -. EMBL; AF31182; AAG35070.1; -. EMBL; BC009726; AAH09726.1; -. EMBL; AC003965; AAB93671.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.252; -. Genew; HGNC:14368; PRSS22.
                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pancreas;
                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteases.
OSS STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE ST
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67 GGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 VPANYSQVE-LGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEAD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 PHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLPLPWVLQEVELRLLGERICQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP-----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                         7 LGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHH 66
                                                                                                                                                                                                                                                                                                                                                                        10 LGGGCLGTFTSLLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GT14_HUMAN STANDARD; PRT; 855 AA.

G9YSYG'S (198801, 2091836; 09HGA3;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Suppressor of tumorigenicity 14 (E3 3.4.21.-) (Matriptase) (Membrane-type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15)
FUMOR associated differentially-expressed gene-15 protein).
ST14 OR PRSS14 OR SMC19 OR TADG15.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
"Molecular cloning of cDNR for matriptase, a matrix-degrading serine protease with trypsin-like activity.";
J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse biochemistry: Use of macromolecular protease inhibitors to dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
                                                                             CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
L -> M (IN REF. 4).
M; EZALZ3BC86E79935 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 SGGPLMCQVDGAMLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQG 291
                                                                   BRAIN-SPECIFIC SERINE PROTEASE 4.
                                                                                                                                                                                                                                                                     Length 317;
                                                                                                                                                                                                                                                                                                       41; Mismatches 123; Indels
                                                                                                                                                                                                                                                                     27.9%; Score 544; DB 1; 39.3%; Pred. No. 3.8e-36;
                                 Hydrolase; Serine protease; Signal.
SIGNAL 1 32 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99303581; Pubmed=10373424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99432178; PubMed=10500122;
TRYPSIN HIS; 1.
TRYPSIN SER; 1.
                                                                                                                                                                                                                      47 L
33731 MW;
                                                                                                                                                                                                                                                                                                         Matches 114; Conservative
                                                                   317
90
141
242
91
227
227
                                                                 33 33 34 241 242 242 242 208 208 208 238 247 47
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Best Local Similarity
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ACT_SITE
ACT_SITE
DISULFID
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CARBOHYD
CONFLICT
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                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                       SEQUENCE
                                                   SIGNAL
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ST14_HUMAN
                                                                   CHAIN
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SEQUENCE FROM N.A.

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rissum=Prostate;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUENCE FROM N.A.

TISSUENCE FROM N.A.

TISSUE=100d, and Muscle;

A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemenn C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Scheuchen M., Madan A., Rodrigues S., Sanchez A. Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Milk;

X MEDLINE=93303582; PubMed=10373425;
A Lin C X., Anders J., Johnson M., Dickson R.B.;
Lin C X., Anders J., Johnson M., Dickson R.B.;
Lin C X., Anders J., Johnson M., Dickson R.B.;

and a Kunitz type serine protease inhibitor from human milk.";

J. Biol. Chem. 274:18237-18242(1999).

J. Biol. Chem. 274:18237-18242(1999).

In Dreast cancer invasion and metastasis. Exhibits trypsin-like in breast cancer invasion and metastasis. Exhibits trypsin-like activity as the Pl site.

C -!- FUNCTION: Type II membrane protein (Probable).

-!- SIMILARITY: Contains 2 CUB domains.

-!- SIMILARITY: Contains 4 LDL-receptor class A domains.
                                   //amaguchi N., Mitsui S.;
//amaguchi n., Mitsui S.;
//amaguchi cloning of a novel transmembrane serine protease expressed
in human prostate.";
                                                                                                                                                                                                                                                              Tanimoto H., Underwood L.J., Wang Y., Shigemasa K., Parmley T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 340-664 FROM N.A.
Cao J., Fan W., Zheng S.;
"Genomic analysis of a novel human serine protease SNC19.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                           Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                  O'Brien T.J.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF118224; AAD42765.2; --
EMBL; AF133086; AAF00109.1; --
EMBL; AF051045; BAB20376.1; --
EMBL; AF057145; AAG15395.1; --
EMBL; BC005826; AAH05826.1; --
EMBL; BC305825; AAH30522.1; --
EMBL; AF283256; AAG13949.1; --
HSSP; P00763; LDPO.
Genew; HGNC:11344; ST14.
                                                                                                                                                                                          [4]
SEQUENCE FROM N.A.
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129 ANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 SKĠNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVĠĠTDADEĠEWPWQVSLHALGQGHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
FER -> GTR (IN REF. 5; AAH05826).
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SIMILARITY).
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R MIM; 606/997; -..

R MEROPS; 501.302; -..

R GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0008286; F:serine-type peptidase activity; TAS.

GO; GO:0006508; P:proteolysis and peptidolysis; TAS.

InterPro; IPR000895; CUB.

R InterPro; IPR001254; Peptidase_SI.

R InterPro; IPR001254; Peptidase_SI.

R InterPro; IPR00124; Peptidase_SI.

R InterPro; IPR001214; Peptidase_SI.

R Pfam; PF00089; TYPPSIN; 1.

R Pfam; PF00089; TYPPSIN; 1.

R PRINTS; PR00021; CUB; 2.

R SMART; SM00042; CUB; 2.

R SMART; SM000192; LDIRECEPTOR.

R SMART; SM00020; TYPP SPC; 1.

R PROSITE; PS00189; LDIRA 1; 2.

R PROSITE; PS00139; LDIRA 1; 2.

R PROSITE; PS00139; LDIRA 1; 2.

R PROSITE; PS00139; LDIRA 1; 2.

R PROSITE; PS00139; TRYPSIN DOM; 1.

R PROSITE; PS00139; TRYPSIN DOM; 1.

R PROSITE; PS00139; TRYPSIN JES; 1.

R PROSITE; PS00139; TRYPSIN JES; 1.

R PROSITE; PS00139; TRYPSIN SER; 1.

R PROSITE; PS00139; TRYPSIN SER; 1.

R PROSITE; PS00139; TRYPSIN SER; 1.

R PROSITE; PS00140; JENERA 1; 2.

R PROSITE; PS00140; JENERA 1; 2.

R PROSITE; PS00140; JENERA 1; 2.

R PROSITE; PS00140; TRYPSIN JES; 1.

R PROSITE; PS00140; TRYPSIN JES; 1.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

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R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS00140; JENERA 2; 2.

R PROSITE; PS0040; JENERA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26143132C01F99C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 SVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE 851
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A -> V (IN REF. 3).
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Isold=Q9Y6M0-2; Sequence=VSP_005389;

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Inoue M., Kanbe N., Kurosawa M., Kido H., \, "Cloning and tissue distribution of a novel serine protease esp-1 from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22881296; PubMed=12975309;
MEDLINE=22881296; PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chan J., Chow B., Cruit C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wisand D., Woods K., Xie M.-H., Yansura D., Godowski P.;
                                                Q9Y6MO; Q9NS34; Q9P2V6; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Testisin precursor (BC 3.4.21.-) (Bosinophil serine protease 1) (BSP-1) (UNQ266/PRO303).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effort to identify novel human secreted and transmembrane proteins:
bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
-!- FUNCTION: Could regulate proteolytic events associated with
testicular germ cell maturation.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI—anchor
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Cervical carcinoma; MEDLINE=99323395; PubMed=10397266; Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L., Normyle J.F., Stuttgen M.A., Douglas M.L., Loveland K.A., Suthtgen M.A., Douglas M.L., Loveland K.A., Sutherland G.R., Antalis T.M., Trestisin, a new human servine proteinase expressed by premeiotic testicular germ cells and lost in testicular germ cell tumors."; Cancer Res. 59:3199-3205 (1999).
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The secreted protein discovery initiative (SPDI), a large-scale
                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 252:307-312(1998).
                                                                                                                                                                                                                                                                                                                                         MEDLINE=20068805; PubMed=10600542;
Inoue M., Itopama T., Xido H.;
"Structural analysis of esp-1 gene (PRSS 21).";
Biochem. Biophys. Res. Commun. 266:564-568(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20461760; Pubmed=11004480;
                                                                                                                                                                                                                                            MEDLINE=99045401; PubMed=9826525;
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Eosinophil;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3)
                                      STANDARD;
                                                                                                                                                                                                                                                                                     human eosinophils.";
                                                                                                                                                  Homo sapiens (Human)
                                      HUMAN
                        FEST_HUMAN
           RESULT 9
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Event=Alternative splicing; Named isoforms=3;

(Potential).
ALTERNATIVE PRODUCTS:

Name=1; Synonyms=L; IsoId=Q9Y6M0-1; Sequence=Displayed; Name=2; Synonyms=S;

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PRINES; PRODUZI; CHYNOTRYBSIN.
PRINES; PRODUZI; CHYNOTRYBSIN.
SMART; SMOOLOJ; TRYPSIN.
PROSITE; PSOOL14; TRYPSIN. HIS; 1.
PROSITE; PSOOL135; TRYPSIN. HIS; 1.
HYDOLTB; PSOOLOJS; TRYPSIN. SER; 1.
HYDOLTB; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen; Alternative splicing; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 AAPLSGP--CGRRVITSRIVGGEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 SGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHC
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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               IsoId=Q9Y6M0-3; Sequence=VSP 005390;
TISSUE SPECIFICITY: Expressed predominantly in premeiotic
testicular germ cells, mostly late pachytene and diplotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
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GO:0005624; C:membrane fraction; TAS.
GO: GO:0005886; C:plasma membrane; TAS.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
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                                                                                spermatocytes. SIMILARITY: Belongs to peptidase family
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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EMBL, AB01329; BAA83520.1; --
EMBL, AB031330; BAR83521.1; --
EMBL, AB031331; BAA89323.1; --
EMBL, AF058301; AAF79019.1; --
EMBL, AF058301; AAF79020.1; --
EMBL, AY359034; AAQ89393.1; --
HSSP; P00763; 1DPO.
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Matches 110; Conserva
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RA MIRAIGO I., OSATO N., SAITOR., SUZUKI H., Yamanaka I., Kiyosawa H.,

RA MIRAIGO I., OSATO N., Basegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hunch C.A., Quackenbush J.,

RA Baldarelli R., Eradpin A., Matsuda H., Batalov S., Beisel K.W.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Granain A., Kawaji H., Kawasawa Y., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Anai A., Kawaji H., Kawasawa Y., Henhard B., Lyons P.A.,

RA Actanai A., Karcchkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Raid J., Ring B.Z.,

RA Ravasi T., Reed D.J., Raid J., Ring B.Z., Ringwald M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Sandelin A., Schneider C., Semple C.A., Sercu M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Sercu M., Sato K.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Rangawa I.,

RA Hirozane-Kishikwaw T., Konno H., Nakamura M., Sakarume N.,

RA Hirazaki T., Waki K., Rawai J., Shibata K., Shinagawa A.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Minayasaki A., Yasaki K., Sasaki D., Shibata K., Shinagawa A.,

RA Minayasi S., Hayashizaki Y.;

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Minayasi S., Rayasaki Z.,

RA Minayasi S., Rayasaki Z.,

RA Minayasi S., Rayasaki Z.,

RA Minayasi S., Rayasaki S.,

RA Minayasi S., Rayasaki S.,

RA Minayasi S., Rayasaki S.,

RA Minayasi S., Rayasaki S.,

RA Minayasi S.,

RA Minayasi S.,

RA Minayasi S.,

RA Mara M., Wate
                                                                                                                                                                                                                          200 NNSMCNHLFLK---YSFRKDIFGDMVCAGNAQGGKDACFGDSGGFLACNKNGLWYQIGUV 256
                                                                                                                                                                                    202 GEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCOGDSGGPLVCEEGGRWFQAGIT 261
84 PETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY----LGNSPYDIA 139
                                                                             142 ILRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mouse matriptase-2: identification, characterization and comparative mRNA expression analysis with mouse hepsin in adult and embryonic
                                                                                                              140 LVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDBALPSPHTLQBVQVAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hooper J.D., Campagnolo L., Goodarzi G., Truong T.N., Stuhlmann H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transmembrane protease, serine 6 (EC 3.4.21.-) (Matriptase-2).
                                                                                                                                                                                                                                                                                             262 SFGFGCGRRNRPGVFTAVATYEAWIRE---QVMGSEPGPAFP 300
                                                                                                                                                                                                                                                                                                                                               257 ŚWGVGCGRPNRPGVYTNISHHFEWIQKUMAÓSGMSQPDPSWP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J;
MEDLINE=22755759; Pubmed=12744720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 373:689-702(2003).
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMS6 MOUSE Q9DBI0;
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                         and uterus.
-!- DEVELOPMENTAL STAGE: Expressed at higher levels from 12.5 dpc to 15.5 dpc with a peak at 13.5 dpc. Expression in the developing liver as well as a restricted set of embrionic epithelial cells of
                                                                                                                                                                                                                                                                                                                                                                "Membrane anchored serine proteases: a rapidly expanding group of cell
                                                                                                                                                                                                                                                                                                                           MEDLINE-22668120; PubMed-12784999;
Netzel-Arnett S., Hooper J.D., Szabo R., Madison E.L., Quigley J.P.,
Bugge T.H., Antalis T.M.;
                                                                                                                                                                                                                                                                                                                                                                             surface proteclytic enzymes with potential roles in cancer.";

Cancer Metastasis Rev. 22:237-258(2003).

-!- FUNCTION: May play a specialized role in matrix remodeling processes in liver (By similarity).

-!- SUBCELLULAR LOCATION: Type II membrane protein.

-!- TISSUE SPECIFICITY: Expressed at highest levels in liver, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR009003; Cys_Ser_trypsin.
IPR002172; LDL_receptor_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001254; PepTidase_S1.
Interpro; IPR001314; PepTidase_S1A.
Pfam; PP00057; 1dl recept_a; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PROUZZ, CHYMOTARPEIN.
PRINTS, PROUZGI, LDLRECEPTOR.
PROSITE; PSO1180, CUB. 1.
PROSITE; PS5068; LDLRA 1; 1.
PROSITE; PS5068; LDLRA 2; 3.
PROSITE; PS5068; LDLRA 2; 3.
PROSITE; PS50144; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
                       MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY240929; AAP69827.1; --
EMBL; AK004939; BAB23584.2; --
EMBL; BC029645; AAH29645.2; --
HSSP; P00763; 1DP0.
MEROPS; S01.308; --
MGD; MG1:1919003; IMPRSS6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000859; CUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                  REVIEW.
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989
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MEDLINE=21153229; PubMed=11231276;
Scarman A.L., Webb G.C.,
Scarman A.L., Antalis T.M.;
Normyle J.F., Antalis T.M.;
"Organization and chromosomal localization of the murine Testisin gene encoding a serine protease temporally expressed during spermatogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   628 KL-WIVFLGKAMRQNSRWPGEVSFKVSRLFLHPYHEEDSHDYDVALLQLDHPVVYSATVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEE-GGRWFQAGIISFGFGCGRRNRPGVF
                                                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
P -> PP (IN REF. 2).
   Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane;
                                                                                                                                                                                                                            SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                       27.3%; Score 533; DB 1; Length 811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Indels
                                                                                                                                                                                                                                                                                                                                                                                   -> PP (IN REF. 2).
32EB3E7C3127801B CRC64;
                                                                                      EXTRACELLULAR (POTENTIAL)
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                                                                                                                                       LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
SERINE PROTEASE.
                                    CYTOPLASMIC (POTENTIAL)
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15-MAR-2004 (Rel. 43, Last annotation update)
Testisin precursor (EC 3.4.21.-) (Tryptase 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8e-35;
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                                                                      (POTENTIAL)
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16-OCT-2001 (Rel. 40, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                     90978 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 110; Conservative
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138
184
                                                                                                                                                                                                                                                                                               216
338
433
453
                                                                                                                                                                                                                                                                                                                                                                                    069
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                                                                                                                                                                                                                                                                                                                                                453
518
690
611 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Q9JHJ7; Q9DA14;
16-OCT-2001 (Rel
                                      109
                     Glycoprotein.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
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                                                                                                                                                                        DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
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CARBOHYD
CARBOHYD
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CARBOHYD
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21085660; PubMed=11217881;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Fara A., Furunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Fara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Andrawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Andrawa T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner, M., Baralov S., Casavanta T.,
Andrawa M., Gasaterland T., Gissi C., King B., Kochiwa H.,
Antell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washlo T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,
Anonstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Saskamoto N.,
Sasaki H., Toyo-oka K., Schoenbach C., Schoart C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYBSIN.
SMART; SM0020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen;
             STRAIN=BALB/C; TISSUE=Testis;
PubMed=11259427;
Wong G.W., Li., Madhusudhan M.S., Krilis S.A., Gurish M.F.,
Rothenberg M.E., Sali A., Stevens R.L.;
"Tryptase 4, a new member of the chromosome 17 family of mouse serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 testicular germ cell maturation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to peptidase family S1. CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 403:063-050 (2001).
-!- FUNCTION: Could regulate proteolytic events associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1916698, Prss21.

GO; GO:0005624; C:membrane fraction; IDA.

GO; GO:0004252; F:serine-type endopeptidase activity; IDA.

InterPro; IPR00103; Cys Ser trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                     Biol. Chem. 276:20648-20658(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 3-324 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001)
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                          proteases.
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Lipoprotein.

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                                                                                                                                                                                                                                                                                                           213 MCNHMYKKP---DFRININGDMVCAGTPEGGKDACFGDSGGPLACDQDTVWYQVGVVSWG
                                                                                                                                                                                                                                                                                             SGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                            FMTNGTLEPPAEWSVLLGVHSQDGPLDG----AHTRAVAAIVVPANYSQVELGADLALLR
                                                                                                                                                                                                                                                                                                                                                                                         LASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                        205 TCQCLYSOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFG
                                                                                                                                                                                                                                                                       22; Gaps
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MEDLINE=99452974; PubMed=10521469;
Worg G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
Friend D.S., Krilis S.A., Stevens R.L.;
"Identification of a new member of the tryptase family of mouse and human mast cell proteases which possesses a novel COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                      (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                 (Potential).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> H (IN REF 3).
W, 56DC59B84F3G3CD4 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tryptase gamma precursor (BC 3.4.21.-) (Transmembrane tryptase).
TPSG1 OR TMT.
                                 FORM (POTENTIAL).
                                          CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                             27.1%; Score 529; DB 1; Length 324; 38.1%; Pred. No. 6.1e-35; Live 53; Mismatches 97; Indels
                                                                                                                                        GPI-anchor amidated asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 FGCGRRNRPGVFTAVATYEAW----IREQVMGSEPGP 297
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                     TESTISIN.
REMOVED IN MATURE
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J. Biol. Chem. 274:30784-30793(1999)
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                          36175 MW;
                                                                                                                                                                                                                                                          Best Local Similarity 38.13
Matches 106; Conservative
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324 AA;
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  TRYG MOUSE
Q9QUL7;
                                                                                                                                                                                                                                                                                                                                                                                           145
                                                                                                     DISULPID
DISULPID
DISULFID
                                                                                                                                                                                      CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
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CHAIN
PROPEP
ACT SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malck J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Froc. Natl. Acad. Sci. U.S.A. 99:16899:16803(2002).
I. TISSUE SPECIFICITY: Expressed in many tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 LEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVE-------LGADLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 CGHPQVSNSGSRIVGGHAAPAGTWPWQASLRHKVHVCGGSLLSPEWVLTAAHCF--SGS
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . )
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPTASE GAMMA LIGHT CHAIN. TRYPTASE GAMMA HEAVY CHAIN.
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EMBL, AF77573; AAF3325.1; --
EMBL, BC02325; AAF3325.1; --
EMSP; P20231; 1AA0.
MESP; P20231; 1AA0.
METOPS; S01.028; --
MGI, MGI.1349391; TPSG1.
InterPro; IPR001254; Pepfidase_S1.
InterPro; IPR001354; Pepfidase_S1.
InterPro; IPR001354; Pepfidase_S1.
If RO0039; LTYPSIN.
PROSITE; PS0240; TRYPSIN.
PROSITE; PS0240; TRYPSIN.
PROSITE; PS02104; TRYPSIN HIS; I.
PROSITE; PS00135; TRYPSIN JER; FALSE NEG.
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311 AA;
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Best Local Similarity
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                                                              261
                                                                               DVKTCSQAYNSP---NGSL-IQPDMLCA---RGPGDACQDDSGGPLVCQVAGTWQQAGVV 232
                                     120 LVGLSSPVALSSQVQPVCLPEASADFYPGMQCWVTGMGYTGEGEPLKPPYNLQEAKVSVV
                                                              GEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGIT
                          LIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-! - SUBCELLULAR LOCATION: Type II membrane protein (Probable).
-! - TISSUE SPECIFICITY: Highly expressed in intestine, kidney, lung, and thymus. Not expressed in skeletal muscle, liver, heart, testis and brain.
                                                                                                                                                                                                                                                                                                      Kim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C., Schwartz R.H.; "Cloning and chromosomal mapping of a gene isolated from thymic stromal cells encoding a new mouse type II membrane serine protease, epithin, containing four LDL receptor modules and two CUB domains."; Immunogenetics 49:420-428(1999).
                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                [1] -
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE CB.174SCUE_Thymus;
MEDLINE=9921640; PubMed=10199918;

Wim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C.,

"im M.G., a gene isolated from '
                                                                                                                                                                                    10-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Epithin).
                                                                                                                                                                                                                                                                                                                                                                               STRAIN≈C.B.17SCID; TISSUE=Thymus;
Kim M.G., Chen C., Cho E.G., Park D., Schwartz R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 23; 321; 325; 343; 409-410 AND C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                 855 AA
                                                                                                 SFGFGCGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                           |:| |||| :||||| : |||| : || || : SWGEGCGRPDRPGVYARVTAYVNMIHHHI 261
                                                                                                                                                                                 (Rel. 38, Created)
(Rel. 40, Last seq
(Rel. 42, Last ann
                                                                                                                                                                 STANDARD;
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VN-SSDYQVHLG-
                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                 15-JUL-1999
16-OCT-2001
10-OCT-2003
                                                                                                                                                                 ST14 MOUSE
                           142
                                                              202
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CGGSLIAPSWVLSAAHCFM--TNGTLEPAAEWSVLLGVHSQD-GPLDGAHTRAVAAIVVP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 CGASLISPDWLVSAAHCEQDDKNEKYSDYTMWTAFLGLLDOSKRSASGVQELKLKRITH 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ARIVGGSNAQPGTWPWQVSLHH-GGGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
SD (GLCNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 855;
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PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Signal-anchor; Glycoprotein; Hydrolase; Serine protease; Transmembrane; Repeat.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 4 LDL-receptor class A domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4F10E84DA2146DD5 CRC64;
                                                                                                                                                                                                                                                                                                               MGD; MGI:1338881; St14.
GO; GO:0005576 C:extracellular; IDA.
GO; GO:009897; C:extrinsic to plasma membrane; IDA.
GO; GO:0008236; F:serine-type peptidase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
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CHARGE RELAY SYS
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InterPro; IPR000803; CVB.
InterPro; IPR001712; LDL_receptor_A.
InterPro; IPR001712; LDL_receptor_A.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; InterPro; InterPro; IPR00131; InterPro; InterPro; IPR00131; InterPro; IPR0131; InterPro; IPR0131; InterPro; IPR0131; IPR0131; IPR0131; IPR03131; IPR03131; IPR03131; IPR03131; IPR03131; IPR03131; IPR03131; IPR03131; IPRA, 1; 2.
IPR03131; IPR0109; IDLRA, 1; 2.
IPR03131; IPR03131; IPRA, 1; 2.
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                                                                                                                                            701 PSFNDFTFDYDIALLELEKSVEYSTVVRPICLPDATHVFPAGKAIWVTGWGHTKEGGTGA 760
129 ANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP 188
                                                                                                              LPWVLQEVELRLLGEATCOCLYSOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Brain;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
"Cloning and characterization of a novel serine protease, mBSSP-4.";
Submitted (JAN-1998) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family Sl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-OCT-2003 (Rel. 41, Last annotation update)
Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
PRSS22 OR PRSS26 OR BSSP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRAIN-SPECIFIC SERINE PROTEASE 4.
CHARGE RELAY SYSTEM (BY SIMILARITY)
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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FBBF03C0C285E7E8 CRC64;
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Signal.
SIGNAL
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Interpro; IPR009003; Cys Ser trypsin.
Interpro; IPR001254; Peptidase_S1.
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HSSP; P00763; 1DPO.
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Q9ER10;
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Conservative

Best Local Similarity Matches 109; Conserv

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                                                                                                                                                                                   60 WQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHT 119
                                                                                                    9 PGQLGAVANSDSYSLYGL------VPSGPARGPPYCGRPEPSARIVGGSNAQPGTWP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89352460; PubMed=2504277;
MEDLINE=89352460; PubMed=2504277;
Wanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
Wanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
Wanderslice Of a unique mode of serine protease activation.";
Biochemistry 28:4148-4155(1989).
-: FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
-: CATMATTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
-: SUBUNIT: Homotetramer.
-: SUBUNIT: Homotetramer.
-: SUBUNIT: Homotetramer.
-: SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                                   179 GDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDT
                                      7 ppalg----gpopsilliluviltstapisaatikvspockroolnrivggedsmdaqwp
                                                                                                                                                              120 RAVAAIVVPANYSQVE-LGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGW
                                                                                                                                                                                                                                                                                                                          239 CQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                                                                                                  mast cell activation.
SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        canis raminaris (109).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO0722; CHYMNTSPEIN.
SMART; SM00020; TIYP. SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ERF; 1.
Hydrolase; Scrine protease; Signal; Glycoprotein; Zymogen.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS, S01.143; ...
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tryptase precursor (EC 3.4.21.59)
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24664; AAA30854.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A32410; A32410.
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANFA
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	'6	P 79 66	L 136 N 118	V 196 V 178	C 249	
(BY SIMILARITY). M (BY SIMILARITY). M (BY SIMILARITY). M (BY CHILARITY). .) (POTENTIAL).	Length 275; Indels 43; Gaps	SLHHGGGHICGGSLIAP 	LDGAHTRAVAAIVVPANYSQVEL 	GWGDVQEADPLPLPWVLQE WGDVHSGTPLPPPFPLKQ	MLCAGYPEGRRDTCQGDSGGPLVC EDMLCAGNSKSDSCQGDSGGPLVC	VMGSEPGPAFPTQP 303
ACTIVATION PEPTIDE (BY SITYPIASE. CHARGE RELAY SYSTEM (BY S CHARGE RELAY SYSTEM (BY S CHARGE RELAY SYSTEM (BY S BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC) (P	Score 514.5; DB 1; Pred. No. 7.2e-34; 27; Mismatches 100;	LYGLVPSGPARGPPYGGRPEPSARIVGGSNAQPGTWPWOVSLHHGGGHICGGSLIAP	SWVLSAAHCEMTNGTLEPAAEMSVLLGVHSODGPLDGAHTRAVAAIVVPANYSQVEL	GADIALLRIASPASLGPAVWPVCLPRASHRFVHGTACMATGWGDVQEADPLPLPWVLQBV	ELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVC ::::	EEGGRWFOAGITSFGFGCGRRNRPGVFTAVATYBAWIREQVMGSEPGFAFFTOP
30 275 121 224 75 2330 211 248 132 30088 M	96 96	ARGPPYCGR	FMTNGTLEP VGPNVVC	ASPASLGPA :: EDPVNVSAH	COCLYSOPG	GITSFGFGC : : GVVSWGEGC
21 31 74 121 224 229 155 188 220 132 275 AA;	26 imilarity 42; Conservative	LYGLVPSGP LGSLVPVSP	SWVLSAAHC : QWVLTAAHC	GADLALLRL : GADIALLEL	ELRLIGEATCQCLYSQPG :::::: KVPIVENSMCDVQY	EEGGRWFQA
PROPEP CHAIN ACT_SITE ACT_SITE ACT_SITE DISULFID DISULFID DISULFID DISULFID CARBOHYD SEQUENCE	Query Match Best Local Similarity Matches 124; Conser	23	80	137	197	250
FT FT FT FT FT FT FT FT FT FT FT FT FT F	Que Bes Mat	çy Dp	Qy Db	QY	Qy Db	QZ QD

Search completed: February 25, 2004, 15:47:56 Job time: 52 secs

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February 25, 2004, 15:36:03; Search time 84 Seconds (without alignments) 1340.952 Million cell updates/sec
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                                                                                                                                                                                   1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF
                                                                                                                                                                                                                                                                                               1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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sp plant: *
sp roden: *
sp virus: *
sp_vertebrate: *
sp_unclassified: *
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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1953
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                                                                                         Run on:
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		Description	Q8nby4 homo sapien	Q99144 mus musculu	Q8bjv6 mus musculu	Q80wm7 mus musculu	Q80x17 mus musculu	Q8r1a6 mus musculu	Q8nf86 homo sapien	Q8n171 homo sapien	Q96rz8 homo sapien	Q8bjr6 mus musculu	Q9pvx7 xenopus lae	Q7t0x2 xenopus lae	088781 rattus ratt	Q9dgr3 xenopus lae	Q8wvc1 homo sapien	Q9bye2 homo sapien
SUMMAKIES		ar	Q8NBY4	Q99L44	Q8BJV6	Q80WM7	Q80X17	QBR1A6	Q8NF86	Q8N171	Q96RZB	Q8BJR6	Q9PVX7	Q7T0X2	088781	Q9DGR3	QBWVC1	Q9BYE2
		DB	4	11	11	11	11	11	4	4	4	11	13	13	11	13	4	4
	* Query	Length	766	339	340	277	331	331	284	327	321	328	389	320	297	317	422	581
	* Query	Match	61.5	32.3	31.4	30.9	30.9	30.7	30.2	30.2	29.8	29.5	29.0					
		Score	1202	630.5	613	603	603	009	590	590	582	570	267	561	560.5	558	540	540
	Result	No.	Н	N	ť	4	ľ	9	7	80	6	10	11	12	13	14	15	16

Q7tml0 mus musculu Q86ym4 homo sapien Q80x21 cattus norv Q9byel homo sapien Q80x23 rattus norv Q80yd8 mus musculu Q80x6 mus musculu Q80x6 mus musculu Q91xc4 mus musculu Q91xc4 mus musculu Q91xc4 mus musculu Q91xc3 mus musculu Q7x411 homo sapien Q92xml ovis aries Q81xm mus musculu Q204x13 mus musculu Q204x13 mus musculu Q204x14 homo sapien Q91x47 mus musculu Q1x410 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q86tm8 homo sapien Q91x77 wenopus eu Q42272 xenopus lae Q8vif2 mus musculu Q96tz6 homo sapien	Q60491 cavia porce Q95me7 oryctolagus O97506 sus scrofa QBr0p5 mus musculu
14 14 14 14 14 14 14 14 14 14 14 14 14 1	11 Q60491 6 Q95ME7 6 O97506 11 Q8R0P5
27.6 27.7	
5388.5 538.5 538.5 538.5 533.7 552.9 633.7 64.5 64.5 64.5 64.5 64.5 64.5 64.5 64.5	473 472.5 470.5 469
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ALIGNMENTS

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1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSG-PARG-PPYCGRP-EPSARIVGGSNAQ-PG
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Best Local Simi
Matches 145;
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                                                    90 MTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPA 149
                                                                                                                                61 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCL 120
                                                                                                                                                              269
                                                                                                                                                                                      121 YSÓPGPFNLTLÓILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGR 180
                                                                           1 MINGILEPPAREMSVILGVHSQDGPLDGAHTRAVARIVVPANYSQVELGADLALLRIASPA 60
                                                                                                        SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPWVLQEVELRLLGEATCQCL
                                                                                                                                                             YSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGR
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane-associated serine protease of the gamma-tryptase/prostasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ, and Swiss; TISSUE=Lung; Verghese G.M., Caughey G.H.; "Molecular cloning and characterization of mouse prostasin, a type
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                            .
0
61.5%; Score 1202; DB 4; Length 766; 100.0%; Pred. No. 2.1e-88; ive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitamura K., Takefumi N., Kimio T.;
"mouse serine protease.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; BC003851; AAH03851.1; -.
EMBL; AR378086; AAL06320.1; -.
EMBL; AR378086; AAL06319.1; -.
EMBL; AB038444; BAB82496.1; -.
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene family.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00702; CHYMOTRYPSIN.
PROSTITE; PS50240; TRYPSIN DOM; 1.

PROSTITE; PS00134; TRYPSIN HIS; 1.

PROSTITE; PS00135; TRYPSIN ERF; 1.

HYGROLASE; PROTESSES; SERIES PROTESSE.
SEQUENCE 339 AA; 36216 NW; BC2DE88BC057AF10 CRC64;
                                                                                                                                                                                                                   270 RNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                                                                                                    GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006299; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                     01-UNN-2001 (TrEMBLrel. 17, Created) 01-UNN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                               339 AA
                                                                                                                                                                                                                                                                                                                                                                             Similar to protease, serine, 8 (Prostasin) PRSS8.
                                                                                                                                                                                                                                                                                                               PRT;
                         Conservative
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1923810; Prss8.
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                            220;
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 Query Match
                Local
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               Best Loca
Matches
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Q99L44
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A the RANCH Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
to 7.70 full-length cONAs.";
Nature 420.563-573(2002).

R Mature 420.563-573(2002).

R MAD: MGI:1923810; Presss.

MGD: MGI:1923810; Presss.

MGD: MGI:1923810; Presss.

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MGD: MGI:1923810; Presss.

MGD: MGI:1928810; Presss.

MGD: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 VVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVTG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                                                    56 WPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE---AYEVKLGAHQLDSYSNDT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 WGDVQEADPLPLPWVLQEVELRLIGEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 TCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 ACOGDSGGPLSCPMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV--AELQP 290
                                                                                                                                                                                                                                                                                                                                                                58 WPWOVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLDGA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
                                                                                                                                                                                       1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSG-PARG-PPYCGRP-EPSARIVGGSNAQPGT 57
                                                                                                                                                                                                                                                                       1 MALRVGLGLGGLEAVT---ILLILGLLQSGLRADGTEASCGAVIQP--RITGGGSAKPGQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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41.5%; Pred. No. 2.2e-41;
tive 46; Mismatches 140; Indels 18;
                                                                                              17;
              Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 RVVPQTQESQPDGHLCNHHPVFSSAAAPKLIRPVLFLPLGLTLGLLSL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 AFPTQPQKTQSD---CLHQTAFLDSAR-ILLRPLSHISVGVSTGTKSL 341
                                                                                              Indels
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Last annotation update)
         DB 11;
    32.3%; Score 630.5; DB 11;
41.7%; Pred. No. 8.7e-43;
tive 48; Mismatches 138;
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MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23,
23,
25,
Query Match
Best Local Similarity 41.7%;
Matches 145; Conservative
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01-MAR-2003
01-OCT-2003
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252

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98 AAEWSVLLG-VHSQDGPLDGAHTRAVAAIVVPANYSQVE-LGADLALLRLASPASLGPAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 CGRPRISGRIVSGQDAQLGRWPWQVSVRENGAHVCGGSLIAEDWVLIAAHCFNQGQSL--
                                   196 VGANVPQGERI---VLPGNLCAGYRRGHKDACQGDSGGPLTCMESGHWVLVGVVSWGKGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 LPVCLPKPGDPLDPGTMCWYTGWGHIGTNQPLPPPFTLQELQVPLIDAETCNTYYQENSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNR
     211 ---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGGRWFQAGITSFGFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 WPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVBLRLLGEATCQCLYSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 PGTEPV---ILEGMLCAGFOEGKKDACNGDSGGPLVCDINDVWIQAGVVSWGSDCALFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGVFTAVATYBAWIREQVMGSEPGPAFPTQPQKTQSDCLHQTAFLDSARILLRP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SEQUENCE FROM N.A.

STRAIN-BALB/c; TISSUE=Brain;

Mong G.W., Yasuda S., Stevens R.L., Li L.;

"Cloning and characterization of mouse tryptase-5 (mT5).";

Submitted (MAR.2003) to the EMBL/GenBank/DDBJ databases.

R MSU, AY266139; AAP3216.1; -.

EMBL, AY266139; AAP3216.1; -.

EMBL, AY266139; AAP3216.1; -.

GO; GO:00004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0006208; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

R Pfan; PF00089; trypsin; 1.

R PROSITE; PS00040; Tryp SPC; 1.

R PROSITE; PS00140; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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(TrEMBLrel. 21, Last sequence update)
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                                                                                                                                                                                                                                                                             331 AA.
                                                                                                                                253 ALPNRPGVYTNVAKYSPWIQARL 275
                                                                                                    268 GRRNRPGVFTAVATYBAWIREQV 290
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01-JUN-2003
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                                                                                                                                                                                                                     113 TVVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVT 172
                                                                                                                                                                                                                                                                                                                                                                          DTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPG 296
                                                                                                                                                                                                                                                                                                                                                                                                    ----AAEWSVLLGVHSQDGPLDGAHTRAVAA--IVVPANYSQVELGADLALLRLASPASL 151
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117 AHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWAT
                                                                                                                                                                                                                                                                      GWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRR
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 PAFPTOPOKTOSD --- CLHQTAFLDSAR-ILLRPLSHISVGVSTGTKSL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 PRVVPQTQESQPDGHLCNHHPVFSSAAAPKLLRPVLFLPLGLTLGLLSL 339
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STRAIN-BALB/C; TISSUE-Testis;

STRAIN-BALB/C; TISSUE-Testis;

Wong G.W., Yasuda S., Li L., Stevens R.L.;

Wong G.W., Yasuda S., Li L., Stevens R.L.;

"Cloning and characterization of mouse tryptase-6 (mT6).";

L Submitted (MRAR-2003) to the EMBL/GenBank/DDBJ databases.

R GO: 00004263; F:chymotrypsin activity; IEA.

R GO: 00004263; F:chymotrypsin activity; IEA.

R GO: 00004265; F:trypsin activity; IEA.

R GO: 00004269; Picroclysis and peptidolysis; IEA.

InterPro: IPR009003; Cys Sar trypsin.

InterPro: IPR001254; Peptidase_SIA.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SEQUENCE 277 AA; 29887 MW; 3310C067573E5E74 CRC64;
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Last annotation update)
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46.4%; Pred. No. 1.1e-40;
tive 30; Mismatches 89;
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Matches 122; Conservative
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Gaps

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PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 GVFTAVATYEAWIREQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 CGRPRTSGRIVSGQDAQLGRWPWQVSVRENGAHVCGGSLIAEDWVLTAAHCFNQGQSL-- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 WPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQ--- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 LPVCLPKPGDPLDPGTMCWVTGWGHIGTNQPLPPPFTLQBLQVPLIDABTCNTYYQBNSI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 AAEWSVLLG-VHSQDGPLDGAHTRAVAAIVVPANYSQVE-LGADLALLRLASPASLGPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPFNLTLQ1LPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 PGTEPV---ILEGMICAGFQQGKKDACNGDSGGFLVCDINDVWIQAGVVSWGSDCALFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 PGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSDCLHQTAFLDSARILLRP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGVYINVSVYISWI-QNTMWNLPMEGRGFSPSISGTPLLGLLTSLSSAFFLLGP 331
                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
                                                                                                                                                                   HSSP; POO741; JAN1.

R MGD; MGI1917064; 2010001P08RiK.

R MGD; MGI1917064; 2010001P08RiK.

R MGC; GO:0004263; F:chymctrypain activity; IEA.

GC; GO:0004295; F:chymctrypain activity; IEA.

R GC; GO:0006208; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00125; CRS Ser Lrypsin.

R InterPro; IPR001254; Peptidase S1.

R PRNINTS; PR00722; CHYMCTRYPSIN.

R PRNINTS; PR00722; CHYMCTRYPSIN.

R PROSITE; PS00240; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS0135; TRYPSIN SR; 1.

R HYdrolase; Protease; Serine protease.

SEQUENCE 331 AA; 35639 MW; C06F6EF2FA261636 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Darrow A.L., Qi J., Andrade-Gordon P., Chen C., "DNA encoding the human serine protease EOS."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RIKEN cDNA 2010001P08 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              30.7%; Score 600; DB 11; I
43.5%; Pred. No. 2.4e-40;
tive 39; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 AA
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                            EMBL; BC024903; AAH24903.1;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.5%
Matches 128; Conservative
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                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                     SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                          010001P08RIK.
                                                                                                                      TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
QBNF86
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157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 GPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CGOPRMSSRIVGGRDGRDGEWPWOASIQHPGAHVCGGSLIAPOWVLTAAHCFPRRAL---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                EMBL, RE536381, AANO4055.1;

QO; GO:0008233; F:chymotrypsin activity; IEA.

QO; GO:0008233; F:peptidase activity; IEA.

QO; GO:0004205; F:trypsin activity; IEA.

QO; GO:0004205; F:trypsin activity; IEA.

QO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00134; Peptidase_S1.

InterPro; IPR00134; Peptidase_S1.

InterPro; IPR00134; Peptidase_S1.

REMNINS; PR00122; CHYMOTRYSIN.

SWART; SW00020; Trypsin; 1.

RENSITE; PS00134; TRYPSIN DOM; 1.

RPOSITE; PS00134; TRYPSIN HIS; 1.

RPOSITE; PS00134; TRYPSIN HIS; 1.

RPOSITE; PS00134; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.

RPOSITE; PS00135; TRYPSIN HIS; 1.
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10cal Similarity 46.3%; Pred. No. 1.3e-39;
hes 119; Conservative 29; Mismatches 99; Indels
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Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protease, serine, 8 (Prostasin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC036866; AAH36846.1; ---
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004235; F:chyptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IRR09003; Cys. Ser trypsin.
InterPro; IRR0124; Peptidase.
InterPro; IRR00124; Peptidase.
FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFEM: FFE
BELONGS TO PEPTIDASE FAMILY SI
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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131 157

97

10;

Length 327; 99; Indels

327 AA; 35106 MW; 60458ED817AC1CF3 CRC64;

SEQUENCE

NON TER

Hydrolase; Protease; Serine protease.

PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN SER; 1.

30.2%; Score 590; DB 4; 46.3%; Pred. No. 1.5e-39; 29; Mismatches

Matches 119; Conservative

75

à d ð

Best Local Similarity

Query Match

38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP 98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP

N

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11;
                                                                                                                                     93 GTLEPAAEWSVLLGVHSQDGPLD---GAHTRAVAAIVVPANYS-QVELGADLALLRLASP 148
                                                                                                                                                                                                                                        36 PYCGRPEPS---ARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTN 92
                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length oDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                            82 GSLN-SSDYQVHL-----GELEITLSPHFSTVRQIILHSSPSGQPGTSGDIALVELSVP
                                                                                                                                                                                                                                                                                                                                    195 DY--PGPGGSILQ--PDMLCA---RGPGDACQDDSGGPLVCQVNGAWVQAGIVSWGEGCG
                                                                                24 PGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRIRRVHVCGGSLLSPQWVLTAAHCF--S
                                                                                                                                                                                                                 149 ASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQC
                                                                                                                                                                                                                                                                                             209 LYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCG
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure and activity of human pancreasin, a novel tryptic serine peptidase expressed primarily by the pancreas.";
J. Biol. Chem. 5:3363-3371(2003).

EMBL; AKO8021; BAC37864.1;
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EMBL; AK162410; AA017162.1;

EMBL; AF542056; AA027572.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2003 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to MARAPSIN precursor (Channel-activating protease 2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6; TISSUE=Bladder;
MEDLINE=22439795; PubMed=12441343;
Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Wolters P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129S6/SvBvTac; Extra Schlessinger D., Nagaraja R.; Bathwaite M., Waeller P., Schlessinger D., Complex Region.", "Genomic Sequence Analysis in the Mouse T-complex Region.", Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                    87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI: 4850123; Mpn.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ger_Lrypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                248 RPNRPGVYTRVPAYVNWIRRHITASGGSESG--YPRLP 283
                                                                                                                                                                                                                                                                                                                                                                           269 RRNRPGVFTAVATYEAWIREQVM---GSEPGPAFPTQP 303
46.0%; Pred. No. 6.6e-39;
iive 35; Mismatches 87
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                  128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein) (Pancreasin)
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  Best Local Similarity
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                    Matches
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiative
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                                                                                                                                                                                                                                130 LVELOGPVIFTNYILPVCLPDPSVIFESGMNCWVTGWGSPSEQDRLPNPRVLOKTAVPII 189
                                                                                                                                                                                                                                                                                                                                                                  261 TSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSE-PGPAFPTQPQK-----TQSD 309
                                                                                                                                                                                                                                                                                                                                                                                 LLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
                                                                                                                                                                83
                                                                                                                                                                                      15 ILRSGTEGARTLRACGHPKMFNRMVGGENALEGEWPWQVSIQRNGIHFCGGSLIAPTWVL 74
                                                                                                                                                                                                                                                                                                                                190 DIPKCNLLYNKDVESDFQLKTIKDDMLCAGFAEGKKDACKGDSGGPLVCLVDQSWVQAGV
                                                                                                                                                                                                                SAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPAN--YSQVELGADLA
                                                                                                                                                                                                                                                                                                                 202 GEATCOCLYSQPGPFNLTLQ-ILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGI
                                                                                                                                                                26 LVPSGP---ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                        22;
                                                                                                               Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'The expression control of xepsin by non-axial and planar
                                                                                                              29.2%; Score 570; DB 11; Length 3 41.3%; Pred. No. 6.2e-38; cive 38; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        posteriorizing signals in Xenopus epiderwis.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-- SINILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; ABO18694; BAA84941.1; -- HSSP; PO0763; 1DPO.
                                                                                      DC0B20F1AB3EB840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00763; 1DPO.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

InterPro; IPR009003; Cys Ser trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

Pfam; PF00099; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epidermis specific serine protease.
XEPSIN.
Pfam, PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPc; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PRO0722, ČĤYMOTRYPSIN.
SMRRT, SMO0020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                       328 AA; 35789 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  310 CLHQTAF-LDSARILLR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                           310 CLAAHAMVLALGALLLR 326
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus
                                                                                                                           Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
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                                                                             Protease.
                                                                                                                                                                                                                84
                                                                                       SEQUENCE
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                                                                                                                Query Match
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Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altaubberg R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casrainci P., Brange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Brange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Brange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raka S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 LTLQILP-----GMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 -SLGYIPDFSFIQEDMVCAGYKEGRIDACOGDSGGPLVCNVNNVWLOLGIVSWGYGCAEP 246
                                                                                                                                                                                                                                                                                                                                                                                                                     98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157
                                                                                                                                                                                                                                                                             38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGVPVISNRIVGGMDSKRGEWPWQISLSYKSDSICGGSLLTDSWVMTAAHCI---DSLD-
                                                                                                                                                                                                              Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                          20;
                                                                                                                                    Length 389;
                                                                                                                                                                                                          Indels
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 389 AA; 42375 MW; B31FB4A2F5D1F6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                          97;
                                                                                                                                    29.0%; Score 567; DB 13; 40.2%; Pred, No. 1.3e-37;
                                                                                                                                                                                                          45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 NRPGVFTAVATYEAWIREQV---MGSEPGPA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 NRPGVYTKVQYYQDWLKTNVPLIVFSEEGPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                          Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae, Xenopus.
NCBI_TaxID=8355;
                                                                                                                                    Query Match
Best Local Similarity
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PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Hydrolase; Protease; Serine protease; Signal.
SIGNAL
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InterPro, IPR001254, Peptidase SI.
InterPro, IPR001314, Peptidase_SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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PRINTS; PR00722; CHYWOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SRR; 1.
Hydrolase; Protease; Serine protease SEQUENCE 317 AA, 34413 MM; EEC78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                     <1 23 PC
24 297 SE
297 AA; 32086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Embryonic serine protease-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| | : | | : | | : | | : | | | : | | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | | : | | | : | | | | : | | | : | | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | : | | | | : | | : | | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 LLGVHSQDGPLDGAHT--RAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 RASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYS----QPG-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ilddmrcagykrekkidacogdsképlýckynntmmoygivsmeikceoanopky
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; Mismatches 107; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Fisher; TISSUB-Brain;
MEDLINE=98.89725; pubMed=9722524;
Davies B.J., Pickard B.S., Steel M., Morris R.G., Lathe
"Serine Proteases in Rodent Hippocampus.";
J. Baol. Chem. 273:23004-23011(1998).
EMBI; AJ005642; CRA06644.1; --.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                 Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56000; AAH56000.1; -.
Hypothetical protein
SEQUENCE 320 AA; 35275 MW; ODC924A312AFA375 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.252; -...
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0003233; F:peptidae activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:trypsin activity; IEA.
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 561; DB 13;
Pred. No. 3.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase_SIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00089, trypsin, 1.
PRINTS, PR00722, CHYMOTRYPSIN.
SMART; SM00020, Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.7%;
                                                 mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                        TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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127
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                                                                                                                                                                                                                                                                                                                                                136 LGADLALLRIASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 VELRILGEATCOCLYSOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRW
                                                                                                                                                                                                             22 SLYGLVPSGPA-----RGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MADDMed=10903452;
MEDLINE=2033741; PubMed=10903452;
Yamada K., Takabatake T., Takeshima K.;
"Isolation and characterization of three novel serine protease genes"
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                         11;
                                                                                                  28.7%; Score 560.5; DB 11; Length 297; 39.4%; Pred. No. 3.3e-37;
                                                                                                                                                         47; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease.
POTENTIAL.
SERINE PROTEASE.
GDA25C6633D6AB55 CRC64;
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Gene 252:209-216 (2000).

EMBL. ABC0846; BAB008216.1; ...

HSSP, P00763; 1DP0.

MEROPS; S01.048; ...

GO; GO:00008233; F:Peptidase activity; IEA.

GO; GO:0008235; F:Peptidase activity; IEA.

GO; GO:0008235; F:Peptidase activity; IEA.

GO; GO:0006289; P:protelysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 FOAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 LLTGIISWGEGCAERNRPGVYTSLLAHRPWVQRIVQG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| | | | : | | | | | PSGC-----GVRLGAYQLYVKNPHEMTVKVDIIYINSEFNGPGTSGDIALLKLSSPIK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 SOPGPFNLT-LOILPGMLCAGYPEGRRDTCOGDSGGPLVCEEGGRWFQAGITSFGFGCGR 269
                                                                                                                                                 PPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCF----M 90
                                                                                                                                                                                           29 PPLCGSPVFSSRIVGGTDTRQGAWPWQVSLEFNGSHIGGGSIISDQWILTATHCIEHPDL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                               151 LGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPWVLQEVELRLLGEATCQCLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 RNRPGVFTAVATYEAWIREQ-VMGSEPGPAFPTQPQKTQSDCLHQTAFLDSARILL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 KNRPGVYTFVPAXETWISERSVISFKP---FTSSSSPSSSVLRASAILLGVSLLL 314
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
Query Match 28.6%; Score 558; DB 13; Length 317; Best Local Similarity 39.2%; Pred. No. 5.6e-37; Matches 116; Conservative 45; Mismatches 119; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Hydrolase; Protease; Serine protease. NON TER 1 1 SEQUENCE 422 AA; 46257 MW; 2C99875D1B58B319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
27.6%; Score 540; DB 4; Length 422;
Best Local Similarity 40.2%; Pred. No. 2.1e-35;
Matches 113; Conservative 39; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; EC018146; AAH18146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R HSDP: P007611, 1AN1.

R HSDP: P007611, 1AN1.

R GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:chymotrypsin activity; IEA.

R GO; GO:0006295; F:crypsin activity; IEA.

R GO; GO:0006509; F:crypsin activity; IEA.

R InterPro; IPR00137; IDL. receptor A.

InterPro; IPR00137; IDL. receptor A.

InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R PRIMTS; PR00157; Idl recept a; 4.

R PRIMTS; PR00767; Idl recept a; 4.

R R RINTS; RR00261; LDLRECEPTOR.

R SMART; SM00192; LDLa; 4.

R RPROFITE; PS00068; LDLA; 4.

R PROSITE; PS00139; LDLA; 2.

R PROSITE; PS00139; LDRA; 1.

R PROSITE; PS00139; LDRA; 1.

R PROSITE; PS00139; LDRA; 1.

R PROSITE; PS00139; LDRA; 1.

R PROSITE; PS00139; LDRA; 1.

R PROSITE; PS00139; LDRA; 1.

R PROSITE; PS00139; LTRYPSIN_INSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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71
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Sequence 66, Appl
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Sequence 11, Appl
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Sequence 6,
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Sequence 21,
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1 MAQKGVLGPGQLGAVANSDS......TKSLVLPWLSPHSLLGLWGF 357
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1: /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-386-642-11

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US-09-907-794A-263

US-09-907-75A-263

US-09-902-775A-263

US-09-027-37-2

US-09-627-37-2

US-09-624-6600-2

US-09-624-6600-2

US-09-624-6600-2

US-09-905-125A-257

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US-09-905-125A-257

US-09-902-775A-257

US-09-903-942A-6

US-09-386-653A-9

US-09-386-600-10

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US-09-386-629-8

US-09-386-629-8

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No.
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65, Appl 2, Appli 2, Appli 4, Appli 5, Appli 19, Appl 11, Appli 6, Appli 6, Appli 6, Appli 7, Appli 7, Appli 6, Appli 7, Appli 6, Appli 7, Appli 8, Appli 9, Appli 9, Appli 9, Appli 9, Appli 1, Sequence 4, Ag Sequence 5, Ag Sequence 53, 7 Sequence 19, 7 Sequence 14, Sequence 21, Sequence 16, 1 Sequence 6, Sequence 4 Sequence 5 Sequence 6 Sequence Sequence Sequence Sequence Sequence US-08-978-404B-5 US-09-80-02-2 US-09-80-002-2 US-09-80-002-2 US-09-90-00-4 US-09-38-642-53 US-09-016-366A-19 US-09-016-366A-19 US-09-016-366A-19 US-09-016-366A-21 US-09-016-366A-21 US-09-01-318-4 US-09-601-318-5 US-09-601-318-6 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7 US-09-601-318-7

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APPLICANT: COLPITY, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: RLASS, MICHAEL R.
APPLICANT: STEWART, KENT D.
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURTENY APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIETCATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONEY, AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                   US-08-944-483-66; Application US/08944483; Sequence 66; Application US/08944483; Patent No. 6212456; GENERAL INFORMATION: APPLICANT: COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS:
LENGTH. 299 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Sequence 7, Application US/09386653A
Patent No. 6458564
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274 GVFTAVATYEAWIREQV 290
                       262 GVYTSVATYSPWIQARV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 316
TYPE: PRT
TRGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Andrade-Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                              CRGANISM: Homo sapiens US-09-386-653A-7
                                                                                           RESULT 3
US-09-386-653A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 GPFNLTLQILPGMLCAGYPEGRRDICQGDSGGPLVCREGGRWFQAGITSFGFGCGRRNRP 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 VHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHR 166
                                                                                                                                                                                                                               ANGLDSYSEDAKVSTLKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANAS 117
                                                                                                                                                                                                                                                                                                       LCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWI 286
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                                                                                                                                  47 IVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLG 106
                                                                                                                                                                                                                                                                                  FVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGM 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 CGQPRMSSRIVGGRDGENDGEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRAL---
                                                                                                                                                           38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
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                                                        30.8%; Score 602; DB 3; Length 299; 41.4%; Pred. No. 2.4e-47; Live 48; Mismatches 120; Indels
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APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Q1, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EDS
TITLE OF INVENTION: Protease EDS
TITLE OF INVENTION: Protease EDS
TITLE OF INVENTION: Protease EDS
TITLE OF INVENTION PROFES: 1999-08-31
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT FILING DATE: 1999-08-31
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.2%; Score 590; DB 4;
46.3%; Pred. No. 2.8e-46;
trive 29; Mismatches 99.
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       No. 6232456e
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Best Local Similarity 46.3'
Matches 119; Conservative
                                                                                                   Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-387-375-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 LPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWLSEH 299
                                                                               Local Similarity
         MOLECULE TYPE:
             ; MOLECULE TYI
US-08-944~483-66
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US-09-387-375-7
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                                                                Query Match
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210 YSQPGPFNLTLQILPG-MLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 NGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPAN--YSQVELGADLALLRLASPA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 RNTSETSL-YQVLLGARQLVQP--GPHAMYARVRQVESNPLYQGTASSADVALVELEAPV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVBLRLLGEATCQCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of BOS zymogen fusion gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.8%; Score 563; DB 4; Length 290; Best Local Similarity 42.2%; Pred. No. 8.6e-44; Matches 117; Conservative 32; Mismatches 114; Indels
APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jian-shen
TITLE OF INVENTION: DNA encoding the novel human serine
TITLE OF INVENTION: Drotease T
FILE REFERENCE: ORT-1032
CURRENT APPLICATION NUMBER: US/09/386,653A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
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APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 RRNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQK 305
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27.98;
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-386-629-7
                                  RESULT 6
US-09-386-642-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EATCQCLYSQPGPFNLTLQ1LPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 RETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDACÓGDSGGPLSCPVEGLWYLTGIVS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 LSAAHCFWINGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLAL 142
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                                                                         3
                                                                                                                                                                                                                                                                                                168 RPPPGTPCRVTGWGSLRPGVPLPEWRPLQGVRVPLLDSRTCDGLYHVGADVPQAERI--- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 CGVPDYKDDDDAAALAAPFDDDDKÍVGGYALBAGOWPWOVSITYEGVHVCGGSLVSEQWV 78
                                                                                                                                       222 ILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVAT 281
                                                                                                                                                                                                                                                                                                                                                                      46 RIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLL 105
                                                                                                                                                                                          106 GVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASH 165
                                                                                                                                                                                                                            108 GALRIGSTSPRILSVPVRRVILPPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGA 167
                                                                                                                                                                                                                                                                   166 REVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQPGPFNLTLQ 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---EPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWV
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                                  28.5%; Score 557; DB 4; Length 316; 45.8%; Pred. No. 3.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER: Patentin Ver. 2.0
                                                                           27; Mismatches
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ORGANISM: Artificial Sequence
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Matches 116; Conservative
                                                         Best Local Similarity *... Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 282 YEAWIREQV 290
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                                    Query Match
Best Local Similarity
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US-09-387-375-9
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TITLE OF INVENTION: Identification and Characterization of the complementary TITLE OF INVENTION: Identification and Characterization of the complementary TITLE OF INVENTION: DNA encoding the novel human serine protease C-E FILLS REFERENCE: ORT-1030
CURRENT APPLICATION NUMBER: US/09/386,629
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFFWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 GAHQLDSYSEDAKVSTLKDIIPHPSYLQEGSQGDIALLQLSRPITFGRYIRPICLPAANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 MVCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 RIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 MLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAW
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Pred. No. 5.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
28.2%; Score 550; DB 4; Length 32
Best Local Similarity 41.2%; Pred. No. 1.6e-42;
Matches 113; Conservative 41; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 IREQVMGSEPGPAFPTQPQKTQSD---CLHQTAF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 IQSKV--TELQPRVVPQTQESQPDSNLCGSHLAF 319
Sequence 11, Application US/09386642
; Patent No. 6420157;
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Ol, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: OFT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT APPLICATION NUMBER: US/09/386,642
; WUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09386629
Patent No. 6426199
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew L.
APPLICANT: Q1, Jenson
APPLICANT: APLAGE-Gordon, Patricia
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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Filvaroff, Ellen
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39.3%;
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Best Local Similarity 39.3;
Matches 114; Conservative
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Sao, Wei-Qiang
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Ashkenazi, Avi
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CRGANISM: Homo Sapien
US-09-907-794A-263
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                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 263
LENGTH: 317
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APPLICANT:
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                                                                                                                                                                                                                                             PLPLPWVLQEVELRLLGEATCQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGD 242
                                                                                                                                                                         127 VPANYSQVE-LGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEAD 185
                                                                                                                                                                                                                                                                             ---itedmicagylegerdacign 241
                                                                                                     67 GGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIV 126
                                                                                                                           70 NGTHHCAGSILITSRWVITAAHCFKDN--LNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE 127
                                                                10 LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPOOLNRVVGGEDSTDSEMPWIVSIOK 69
                                 7 LGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
                                                                                                                                                                                                                                                                                                                                      SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
 12;
Mismatches 123; Indels
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: US 60/143,048
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PRIOR FILING DATE: 1999-07-26
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerritsen, Mary B.
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Stewart, Timothy I
Tumas, Daniel
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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   Conservative
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Gerber,
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127 VPANYSQVE-LGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEAD 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 PHPVYSWKEGACADIALVKLERSIQFSERVLPICLFDASIHLPPNTHCWISGWGSIQDGV 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPNIVSLQK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 PLPLPWVLQEVELRLLGEATCQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 SGGPLMCQVDGAWILAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQG 291
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLILNG DATE: 1999-11-30
PRIOR PLILNG DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLILNG DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 1999-12-06
PRIOR PLILNG DATE: 1999-12-16
PRIOR PLILNG DATE: 1999-12-20
PRIOR PLILNG DATE: 1999-12-20
PRIOR PLILNG DATE: 1999-12-20
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PRIOR PLILNG DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILNG DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR PLILNG DATE: 2000-01-05
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Patent No. 6664376
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
       243 SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                     242 SGGPLMCQVDGAMILAGIISWGEGCAERNRPGVXISLSAHRSWVEKIVQG 291
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PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
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PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/30911
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FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Hillan, Kenneth,
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Gao, Wei-Qiang
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PRIOR APPLICATION NUM
PRIOR FILING DATE: 20
                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                          RESULT 10
US-09-902-775A-263
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                                                                                                                                             APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembran
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-09-09
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
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PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
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PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
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APPLICATION NUMBER: US 60/143,048
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39.3%;
                                                                       Margaret Ann
art, Timothy A.
                                             Paoni, Nicholas F.
Mather, Jennie P.
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Best Local Similarity 39.34
Matches 114; Conservative
                                                                                               Stewart, Timof
Tumas, Daniel
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ORGANISM: Homo Sapien
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APPLICANT:
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189 LPWVLQEVELRLIGERITCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL- 247
                                                                                           248 VCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIRE 288
                                                                                                                    811 SVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 VCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIRE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 SVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%; Score 540; DB 4;
40.2%; Pred. No. 4.8e-41;
Live 39; Mismatches 95
                             Sequence 2, Application US/09654600A
Patent No. 6649741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 40.2%
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: TADG-15 US-09-644-600-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-09-654-600A-2
                                                                                                                                                                                                  RESULT 12
US-09-644-600-2
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APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                         67 GGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                     70 NGTHHCAGSLLTSRWVITAAHCFKDN--LNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE 127
                                                                                                                                                                                                                                                                                                                                  69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides OTHER INFORMATION: 23 to 2589 of Sequence 1
                                                                                                                                                                                                                                                                                                                  10 LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEMPWIVSIQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         581 SKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLPLPWVLQEVELRLLGEATCQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SARIVGGSNAQPGTWPWQVSLHH-GGGHI
                                                                                                                                                                                                                                                                                    7 LGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQG 291
                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                    Length 317;
                                                                                                                                                                                                27.9%; Score 544; DB 4; Length 31 39.3%; Pred. No. 5.4e-42; Live 41; Mismatches 123; Indels
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 263
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-027-337-2; Sequence 2, Application US/09027337B; Patent No. 5972616
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Best Local Similarity 40.2
Matches 113; Conservative
                                                                                                                                                                                                Query Match 27.9
Best Local Similarity 39.3
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 ARGPPYCGRPEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                           TYPE: PRT
ORGANISM: Homo Sapien
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                                                                                                                                                       US-09-902-775A-263
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LENGIH: 85
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----OITPRMMCVGFLSGGVDSCOGDSGGPLS 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 CGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SARIVGGSNAQPGTWPWQVSLHH-GGGHI
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                                                                                                                                                                                                                                                                       Sequence 2, Application US/09644600
Fatent No. 6451500
GENERAL INFORMATION
THORMATION THOORATION
THE OF INVENTION: Tanimoto, Hirotoshi
TILE OF INVENTION: TADG-15: An Extracellular Serine Protease
TILE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT FILING DATE: 2000-08-23
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
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APPLICANT: O'BRIEN, Timothy J.
APPLICANT: O'BRIEN, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/654,600A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
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Gaps

19;

Indels

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84 FETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY----LGNSPYDIA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 FMTNGTLEPAAEWSVLLG-VHSQDG--PLDGAHTR-AVAAIVVPANYSQVELG---ADLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 LLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AAPLSGP--CGRRVITSRIVGGEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 GEATCOCLYSOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.4%; Score 534.5; DB 3; Best Local Similarity 39.0%; Pred. No. 4e-41; Matches 110; Conservative 53; Mismatches 100;
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
                                                                                                                                                                                                                                                                                                       CLONE: 789927
SEQUENCE DESCRIPTION: SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 257, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEPHONE: 650-855-0555
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Timothy A.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Stewart, Timothy I
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen, Mary B
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                                                                                                                                                                                                               TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-907-794A-257
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 CGASLISPNWIVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISH 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 LPWVLQEVELRLIGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 PFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SARIVGGSNAQPGTWPWQVSLHH-GGGHI
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                              Length 855;
                                                                                                                                                                                                                                                                                                                                           Similarity 40.78; Score 540; DB 4; Length 85 Similarity 40.78; Pred. No. 4.8e-41. Conservative 39; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 VCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIRE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 SVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown>
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NAME: Mohan-Peterson, Sheela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Dr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                         39;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
      PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                ; OTHER INFORMATION: TADG-15
US-09-654-600A-2
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 ARGPPYCGRPEP-
                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                      1998-02-20
NUMBER OF SEQ ID NOS:
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US-09-008-271A-3
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 113;
                                                                                          SEQ ID NO 2
LENGTH: 855
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Best Local
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140 LVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVIGWGYIKEDEALPSPHTLQEVQVAII 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 FMTNGTLEPRAEWSVLLG-VHSQDG--PLDGAHTR-AVAAIVVPANYSQVELG---ADLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 FETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY----LGNSPYDIA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 LIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.4%; Score 534.5; DB 4; Length 314;
Best Local Similarity 39.0%; Pred. No. 4e-41;
Matches 110; Conservative 53; Mismatches 100; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 SFGFGCGRRNRPGVFTAVATYEAWIRE---QVMGSEPGPAFP 300
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PRIOR PEDLICATION NUMBER: PCT/USO/04414
PRIOR PELLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PELLING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-16
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Job time : 46 secs
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; ORGANISM: Homo Sapien
US-09-907-794A-257
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February 25, 2004, 15:49:38; Search time 641 Seconds (without alignments) 117.600 Million cell updates/sec
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1953
1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NBW_PUB_pep:*
3: cgn2_6/ptodata/1/pubpaa/US06_PUBGOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBGOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Description	Sequence 111, App Sequence 2, Appli	Sequence 86, Appl	Sequence 262, App	Sequence 125, App	Sequence 2, Appli	Sequence 86, Appl	Sequence 87, Appl	Sequence 26, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 89, Appl	Sequence 8, Appli	Sequence 36. Appl
SUMMARIES	US-09-948-615-111 US-09-948-094-2	US-10-176-847-86	US-10-097-340-262	US-10-074-566-125	US-10-109-616-2	US-10-051-874-86	US-10-051-874-87	US-10-051-874-26	US-10-041-400A-7	US-10-041-264A-7	US-10-042-091A-7	US-10-051-874-89	US-10-311-035-8	US-10-221-097-36
DB		14	14	15	14	15	15	15	13	13	13			14
% Query Match Length DB	818 343	343	343	343	339	342	342	280	284	284	284	285	346	255
% Query Match	77.1	35.3	35.3	35.3	32.1	31.8	31.7	30.2	30.2	30.2	30.2	29.9	29.8	29.5
Score	1505	069	069	069	627.5	621	620	590	590	290	590	583.5	582.5	575.5
Result No.	. 4 2	ĸ	4	ហ	9	7	8	6	10	11	12	13	14	15

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Gaps

97 97

38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP 98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP

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157 157

158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN 217

Applications of the property o	App App App App App App App
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38 CGRPEPSARIVGGSNAQPGTWPWQVSIHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
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                   Patent No. US20020064856A1

Patent No. US20020064856A1

GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY

APPLICANT: CARNEBEL, SEAN

APPLICANT: CHARYDCZAK, GLEN

APPLICANT: CHARYDCZAK, GLEN

APPLICANT: CHARYDCZAK, GLEN

APPLICANT: SUDARSANAM, SUCHA

ITLE OF INVENTION: NOVEL PROTEASES

FILE REFERENCE: 038602/1214

CURRENT FILING DATE: 2001-06-26

PRIOR FILING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 150

SOFTWARE: PATENT NOS: 150

SOFTWARE: PATENT NOS: 150

SOFTWARE: PATENT NOS: 150

SOFTWARE: PATENT NOS: 150

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SOFTWARE: PATENT NOS: 150
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Best Local Similarity 100.
Matches 272; Conservative
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ORGANISM: Homo sapiens
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US-09-888-615-111
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Gaps

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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TGWGDVQBADPLPLPWVLQBVELRLLGBATCQCLYSQPGPFNLTLQILPGWLCAGYPBGR 235
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                                                                                                                                                                                                                                                                                                                                                    54 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE 110
                                                                                                                                                                                                                                                                                                                                                                                                          116 GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG---LLSPWLSEH 343
                                                                                                                                                                                                                                           1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
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                                                                                                                                                                                                                                                                                                                          56 GTWPWQVSLHHQQGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLD
                                                                                                                                                                 Length 343;
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                                                                                                                                                Best Local Similarity 43.6%; Pred. No. 1.1e-51; Matches 156; Conservative 49; Mismatcher
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PRIOR PELICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR PELICATION NUMBER: 60/325,149

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR PELING DATE: 2001-03-24

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001/03/24,967

PRIOR FILING DATE: 2001/09/26

PRIOR FILING DATE: 2001/09/26

PRIOR FILING DATE: 2001/09/26
NUMBER OF SEQ ID NOS: 112
SOFWARE: FastSEQ for Windows Version
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 262, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORZISEY
Peter OLANDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: John MONAHAN APPLICANT: Manjula GANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peter VEIBY
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Karen GLATT
                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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US-10-097-340-262
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 TGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR 235
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                                                                         LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT 277
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            Sequence 2, Application US/09948094
Sequence 2, Application US/09948094
Batent No. US20020090625A1
GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Mong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
FILE REPERENCE: 81994/828423
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
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                                                                                                                                                               AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                                                                    278 AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
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Matches 156; Conservative
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ORGANISM: Homo sapiens
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US-10-176-847-86
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US-09-948-094-2
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58 WPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
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TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL
TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAPI) GENE DISRUPTIONS
TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAPI) GENE DISRUPTIONS
FILE REPERENCE: R-490
CURRENT APPLICATION NUMBER: US/10/109,616
CURRENT FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 2.
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41.4%; Pred. No. 2.9e-46;
tive 48; Mismatches 139;
                                                                                                                                                                                                                                                                              35.3%; Score 690; DB 15;
43.6%; Pred. No. 1.1e-51;
                                                                                                                                                                                                                                                                                                                          49; Mismatches
PRIOR APPLICATION NUMBER: 60/291,766
PRIOR PILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/314,007
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 132
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 125
LENGTH: 343
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US-10-109-616-2
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                          TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                     US-10-074-566-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 GAHTRAVAAIVVPANYSQVELGADIALIRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDICOGDSGGPLVCEEGGRWFQAGIISFGFGCGRRNRFGGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                                                                                                                                                                                                                  1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP 55
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 GPAFPTOPOKTOSD---CLHOTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
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APPLICANT: Gorman, Linda
APPLICANT: Gasev, Vladimir Y.
APPLICANT: Padigaru, Meralidhara
APPLICANT: Patturajan, Mesea
APPLICANT: Shenoy, Suresh G.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Pollyeptides and Polynucleotides Encoding Same
FILE REFERENCE: 15966-556 CIP1
CURRENT APPLICATION NUMBER: 2002-02-18
PRIOR PLLING DATE: 2002-02-19
PRIOR FILING DATE: 2000-07-05
                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                                                        49; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                           35.3%; Score 690; DB 14; 43.6%; Pred. No. 1.1e-51;
         PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 343
TYPE: PRI
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PRIOR PILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/144,722
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/276,994
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/280,898
PRIOR FILING DATE: 2001-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/332,241
FILING DATE: 2001-11-14
APPLICATION NUMBER: 60/288,062
FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 125, Application US/10074566 Publication No. US20030207348Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shimkets, Richard A. APPLICANT: Fernandes, Elma R.
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.69
Matches 156; Conservative
                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-097-340-262
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
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Tchernev, Velizar T
Zerhusen, Bryan D
FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rattus norvegicus
US-10-051-874-86
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Best Local Similarity 40.8
Matches 144; Conservative
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US-10-051-874-87
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TITLE OF INVENTION: PROTEINS, POLYNUCLECTIDES ENCODING THEM AND METHODS OF
ITILE OF INVENTION: USING THE SAME
                                                                                                                                                                                                                                  233 ACCGDSGGPLSCPMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV--AELQP 290
                                                                                                                                                                                                238 TCOGDSGGPLVCEEGGRWFOAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGP 297
                                                    118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
 56 WPWQVSITYDGNHVCGGSLVSNKWVVSAAHCPPREHSRE---AYEVKLGAHQLDSYSNDT 112
                                                                             113 VVHTVAQIITHSSYREEGSQGDIAFIRLSSPVTFSRXIRPICLFAANASFINGLHCTVTG
                                                                                                                            WGDVQEADPLPLFWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRD
                                                                                                                                                         298 AFPTQPQKTQSD---CLHQTAFLDSAR-ILLRPLSHISVGVSTGTKSL 341
                                                                                                                                                                                                                                                                                               291 RVVPQTQESQPDGHLCNHHPVFSSAAPKLLRPVLFLPLGLTLSL 338
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CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2002-09-25
PRIOR PILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-27
PRIOR PLICATION NUMBER: 60/325,306
PRIOR PLICATION NUMBER: 60/325,307
PRIOR APPLICATION NUMBER: 60/202,587
PRIOR PILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/202,587
PRIOR APPLICATION NUMBER: 60/202,587
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 86, Application US/10051874 Publication No. US20040005557A1 GENERAL INFORMATION:
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Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
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Smithson, Glennda
Baumgartner, Jason C
Herrman, John L
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Zerhusen, Bryan D
Millet, Isabelle
Miller, Charles E
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Shimkets, Richard A
Pena, Carol EA
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Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
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Shenoy, Suresh G
Shenoy, Stacie J
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Stone, David J
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Ellerman, Karen
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58 WPWQVSLHHCGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 HTRAVAALVVPANYSQVELGADLALLRIASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 VVHTVAQIISHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLBAANASFPNGLHCTVTG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQKGVI,GPGQLGAVANSDSYSLYGLVPS--GPARGPPYCGRP-EPSARIVGGSNAQPGT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 WGDVQEADPLPLPWYLQEVELRLIGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 TCCCDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%; Score 621; DB 15;
40.8%; Pred. No. 1.1e-45;
tive 50; Mismatches 139;
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/291,672
PRIOR PLING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/330,336
PRIOR PRIOR DATE: 2001-18
PRIOR PAPLICATION NUMBER: 60/265,530
PRIOR PRIOR DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/261,376
PRIOR PRIUNG DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTING DATE: 2014-01-16
NUMBER OF SEQ ID NOS: 269
TENGTHER PATENTING DATE: 2014-01-16
NUMBER OF SEQ ID NOS: 269
TENGTHER PATENTING DATE: 2014-01-16
NUMBER OF SEQ ID NOS: 269
TENGTHER PATENTING DATE: 217
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spytek, Kimberly A Boldog, Ferency Vernet, Corine AM Li, Li Shenoy, Suresh G Casman, Stacie J Guo, Xiaojia Sasha Edinger, Shlomit R MacDougall, John R Malyankar, Uriel M Patturajan, Meera Shimkets, Richard A Boldon, Kimberd A
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233 ACQGDSGGFLSCPIDGLWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV--AELQP 290
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TITLE OF LINGWILD.

CURRENT APPLICATION NUMBER: US/10/051,874

CURRENT FILING DATE: 2002-09-25

PRIOR APPLICATION NUMBER: 60/268,595

PRIOR PILING DATE: 2001-02-14

PRIOR PILING DATE: 2001-09-27

PRIOR PILING DATE: 2001-09-27

PRIOR PILING DATE: 2001-09-27

PRIOR PILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: 60/22,409

PRIOR FILING DATE: 2001-01-18

PRIOR PILING DATE: 2001-01-08-06

PRIOR APPLICATION NUMBER: 60/26,75777

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/29,7777

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/291,672

PRIOR APPLICATION NUMBER: 60/30,336

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/30,336

PRIOR APPLICATION NUMBER: 60/20,336

PRIOR APPLICATION NUMBER: 60/20,530

PRIOR APPLICATION NUMBER: 60/20,530
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APPLICATION NUMBER: 60/265,530
FILING DATE: 2001-01-31
APPLICATION NUMBER: 60/261,376
FILING DATE: 2001-01-16
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APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Liu, Xiaohong
APPLICANT: Blerman, Karen
APPLICANT: Rothenberg, Mark
APPLICANT: Rothenberg, Mark
APPLICANT: Rothenberg, Mark
APPLICANT: Rothenberg, Catherine E
TITLE OF INVENTION: PROTEINS, POLYN
TITLE OF INVENTION: PROTEINS, POLYN
TITLE OF INVENTION: USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tcherney, Velizar T
Zerhusen, Bryan D
Millet, Isabelle
Millet, Charles E
Lepley, Denise M
Smithson, Glennda
Baungartner, Jason C
Herrman, John A
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
Vernet, Corine AM
Li, Li
Shenoy, Suresh G
Casman, Stacie J
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Shimkets, Richard A
Pena, Carol EA
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MacDougall, John R
Malyankar, Uriel M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 VVHTVAQIISHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASPNGLHCTVTG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 WGHVAPSVSLOTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGGKD 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFLICANT: SUCHE, DAYLE OF TATLLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES TITLE OF INVENTION: USING THE SAME TITLE OF INVENTION: USING THE SAME TITLE REPERENCE: 2102-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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PRIOR FILING DATE: 2001-03-17
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-31
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PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
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PRIOR FILING DATE: 2001-01-31
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Kekuda, Ramesh
Taupier Jr, Kaymond J
Gerlach, Valerie
Grosse, William M
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Herrman, John L
Peyman, John A
                                                                                   Lepley, Denise M
Smithson, Glennda
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CRGANISM: Rattus norvegicus
US-10-051-874-87
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Stone, David J
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Best Local Similarity 40.8
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Liu, Xiaohong
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LENGTH: 342
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APPLICANT:
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POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
298 AFPTQPQXTQSD---CLHQTAF-LDSARILLRPLSHISVGVSTGTKSLVLPWL 346
                                      291 RAVPOTÇESQPDGHLCNHHPVFNLAAAQKLSRPILFIPLFLSLTLGLFSL---WL
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205 QAERI----VLPGSLCAGYPQGHKDACQGDSGGPLTCLQSGSWYLVGVVSWGKGCALPNRP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLIGEATCQCLY----SQP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 GPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 CGQPRMSSRIVGGRDGFWFWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRFAL---
205 QAERI----VLPGSLCAGYPQGHKDACQGDSGGPLTCLQSGSWVLVGVVSWGKGCALPNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
30.2%; Score 590; DB 13; Length 284;
Best Local Similarity 46.3%; Pred. No. 4.3e-43;
Matches 119; Conservative 29; Mismatches 99; Indels 10
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APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Al John Son
APPLICANT: Al John Son
APPLICANT: Al John Son
APPLICANT: Al John Son
APPLICANT: Al John Son
FILE REPERENCE: ORI-1031
CURRENT APPLICATION NUMBER: US/10/042,091A
CURRENT FILING DATE: 2002-01-08
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                        APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Procease EOS
                                                                                                                                                                                                                                                                                                                                                                              CURENT APPLICATION NUMBER: US/10/041,264A
CURENT APPLICATION NUMBER: US/10/041,264A
CURENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10042091A Publication No. US20020142447A1 GENERAL INFORMATION:
                                                                                                                                                                                                           Sequence 7, Application US/10041264A Publication No. US20020142446A1
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                                                                                                262 GVYTSVATYSPWIQARV 278
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                                                                        274 GVFTAVATYEAWIREOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-10-041-264A-7
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 AAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 QAERI---VLPGSLCAGYPQGHKDACQGDSGGPLTCLQSGSWVLVGVVSWGKGCALPNRP 261
                                                                                                                                                                                                                                                                                                                                                  98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157
                                                                                                                                                                                                                                                                 38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP 97
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                                                                                                                                                                                                                                                                                                                                                                            158 VCLPRASHREVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Gaps
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                                                                                                                                                                                                                              Gaps
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30.2%; Score 590; DB 13; Length 284;
Best Local Similarity 46.3%; Pred. No. 4.3e-43;
Matches 119; Conservative 29; Mismatches 99; Indels 1
                                                                                                                                                                                     Length 280;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Oi, Jenson
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
FILE REPERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                     Query Match 30.2%; Score 590; DB 15; Best Local Similarity 46.3%; Pred. No. 4.2e-43; Matches 119; Conservative 29; Mismatches 99;
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Publication No. US20020110895A1
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262 GVYTSVATYSPWIQARV 278
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                        NUMBER OF SEQ ID NOS: 269
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 280
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                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-051-874-26
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BAUGHN, Mariah R.
NGUYEN, Danniel B
LEE, Ernestine A.
TITLE OF INVENTION:
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US-10-311-035-8
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APPLICANT:
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                                                                                                                                                                                                                                                                              158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQP 213
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TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
                                                                                                                                                      97
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                                                                                                                                                      38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                          28 CGQPRMSSRIVGGRDGEWPWQASIQHPGAHVCGGSLIAPQWVITAAHCFPRRAL---
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                                                                                                                         Gaps
                                                                                                                         10;
                                                                                       Length 284;
                                                                                                                         Indels
                                                                                                                         :66
                                                                                         Query Match
30.2%; Score 590; DB 13;
Best Local Similarity 46.3%; Pred. No. 4.3e-43;
Matches 119; Conservative 29; Mismatches 99;
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Publication No. US20040005557A1
APPLICANT: Padigaru, Muralidhara
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Mezes, Peter D
Kekuda, Ramesh
Taupier Jr, Raymond J
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
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Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
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Herrman, John L
Peyman, John A
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Zerhusen, Bryan D
Millet, Isabelle
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Lepley, Denise M
Smithson, Glennda
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GroßBe, William M
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Stone, David J
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                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-042-091A-7
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US-10-051-874-89
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173 WGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGGKD 232
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29.9%; Score 583.5; DB 15; Length
Best Local Similarity 43.3%; Pred. No. 1.6e-42;
Matches 127; Conservative 39; Mismatches 116; Indels
               TILLE OF LINGWILLON: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR APPLICATION NUMBER: 60/225,306
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR FILING DATE: 2001-09-27
PRIOR PELLING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-28
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/276,477
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/291,672
PRIOR APPLICATION NUMBER: 60/291,672
PRIOR PELLING DATE: 2001-05-17
PRIOR PELLING DATE: 2001-05-17
PRIOR PELLING DATE: 2001-05-17
PRIOR PELLING DATE: 2001-01-10
PRIOR PLING DATE: 2001-01-10
PRIOR PLING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR PELLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR PELLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR PELLING DATE: 2001-01-16
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APPLICANT: YUE, Henry.
APPLICANT: ELLIOTT, Vicki
APPLICANT: GANDHT, Ameena R.
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: TRIBOLLEY, Catherine M.
APPLICANT: TRIBOLLEY, Catherine M.
APPLICANT: DELEGEANE, Angelo M.
USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10311035 Publication No. US20040023243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Mus musculus
US-10-051-874-89
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220 IQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAV 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 IVGGSUAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 VHSQDGPLDGAHTRAVAAIVVPAN----YSQVELGADLALLRLASPASLGPAVWPVCLP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 --ROYRCPETRRITRS----ALPIRKRRRAYNHYSOGSDLALLOLAHPIT----HIPLCLP
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             FILE REFERENCE GEOVER
CURRENT APPLICATION NUMBER: US/10/221,097
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PRILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOCTWARRE: FRELSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 255
TYPE: PRI
ORGANISM: Homo sapiens
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Best Local Similarity 43.7;
Matches 128; Conservative
REFERENCE:
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### APPLICANT: REDRY, RODGE

### APPLICANT: REARNEY, Liam

### APPLICANT: KEARNEY, Liam

### TITLE OF INVENTION: Proceases

### TITLE OF INVENTION: Proceases

### TITLE OF INVENTION: Proceases

### CURRENT PLING DATE: 2000-102-10

### FILM APPLICATION NUMBER: 60/212,336; 60/213,955; 60/216,821; 60/218,946

### RICK APPLICATION NUMBER: 60/212,336; 60/215,396; 60/216,821; 60/218,946

### RICK APPLICATION NUMBER: 60/212,2000-07-07; 2000-07-07

### SOFTWARE: PERL Program

### SOFTWARE: PERL Program

### SOFTWARE: PERL PROGRAM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GGGHICGGSLIAPSWVLSAAHCFMINGTLEPAAEWSVLLGVHSQDGPLD---GAHTRAVA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023243A1 2256251CD1
US-10-311-035-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.8%; Score 582.5; DB 1 43.8%; Pred. No. 2.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Agarwal, Pankaj
APPLICANT: Murdock, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
                                 CHANLA, Narinder K.
CHANLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
ARVIZU, Chandra S.
TANC, Y. Toom
WALSH, Roderick T.
AZIMZAI, Yalda
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Matches 133; Conservative
                HAFALIA, April
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ORGANISM: Homo sapiens
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CQ31_1/05PQ spool p/US10037417/runat_24022004_101038_17447/app_query.fasta_1.519
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                                                                            February 25, 2004, 15:51:34; Search time 3779 Seconds (without alignments) 4094.592 Million cell updates/sec
                                                                                                                               US-10-037-417-46
1953
1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                    using frame_plus_p2n model
                                                                                                                                                                                                                                                                3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AK075142 Homo sapi AX42934 Sequence BD125219 Primer fo BD12648 Primer fo AX342936 Sequence AC009088 Homo sapi AX335777 Sequence BC01462 Homo sapi AX335777 Sequence AX40567 Sequence AX40567 Sequence AX40567 Sequence AX40567 Sequence AX44697 Sequence AX44697 Sequence AX46567 Sequence AX40567 Sequence AX46567 Sequence AX40567 Sequence AX40652 Sequence AX16629 Sequence

AX512287 Sequence AX512289 Sequence AX480096 Sequence AX480935 Sequence BD127529 Primer fo

SUMMARIES

ALIGNMENTS

AY335911 Mus muscu BC003851 Mus muscu AR038244 Mus muscu AF38085 Mus muscu AF188613 Mus muscu AF202076 Rattus no BC061800 Rattus no AC124461 Mus muscu AC093175 Mus muscu AC093175 Mus muscu

AY262280 Mus muscu BC024903 Mus muscu AX676264 Sequence

Homo sapi Sequence

AR256990 AF536382 BC062334

AX823252 Sequence BC056000 Xenopus

AY266139 Mus muscu AX675581 Sequence AC117170 Rattus no

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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U., Rothenberg,M., Stone,D., Boldog,F., Shenoy,S. and Anderson,D. Proteins and nucleic acids encoding same

Patent: WO 02053742-A 45 11-JUL-2002;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                           GlnIleLeuproGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAspThrCysGln
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                                                CTGGGCGAGGCCACCTGTCAATGTCTCTACAGCCAGCCCGGTCCCTTCAACCTCACTCTC
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                                LeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyProPheAsnLeuThrLeu
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Conservative:
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61 GlnValSerleuHisHisGlyGlyGlyHisIleCysGlyGlySerleuIleAlabroSe.	TrpServalle											

PAT 13-FEB-2002

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DNA

AX360096 2457 bp Sequence 52 from Patent W00200860.

RESULT 3
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                                                                                                      owman,G., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. and tarydczak,G.
wel proteases
trent: WO 0200860-A 52 03-JAN-2002;
igen, Inc. (US)
Location/Qualifiers
1. 2457
/organis="Homo sapiens"
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JP 2002017375-A/2960
22-JRN-2002
72-JNL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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1 (bases 1 to 2810)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                    178 TrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGlu 197
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412 GCCGACCTGGCCTGCGCCTTGGCCTCACCCGCCTGGGCCCCGCCGCGTGTGGCCT
                                    ValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
                                                      YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2960
PD 22-JAN-2002
PF 07-JUL-2000 JP 200253172
PF TOSHIO OTA, TETSUO NISHIKANA, TAKAO ISOGAI, KOJI HAYASH
PI ISHII,
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/mol_type="genomic DNA"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yue, H., Azimzai, Y., Kallick, D.A., Baughn, M.R., Griffin, J.A., Swarnakar, A., Lal, P.G., Walia, N.K., Hafalia, A.J., Gandhi, A.R., Au-Young, J., Elliott, V.S., Ramkumar, J., Thangavelu, K., Lu, Y., Warren, B.A., Lu, D.A., Lee, E.A., Tribouley, C.M., Arvizu, C., Delegeane, A.M., Yao, M.G., Khan, F.A. and Sanjanwala, M.M. Protein modification and maintenance molecules

Patent: WO 0246389-A 31.33-JUN-2002;
                                                                                                                                   832 GCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCTGGGCCT
                                                                                                    AlavalalaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluProGlyPro
                                  258 AlaglyileThrSerPheGlyPheGlyCysGlyArgArgAshArgProGlyValPheThr
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                                                                                                                                                                                                       892 GCCTTTCCCACCCAGCCCCAGAAGACCCAGTCAGAT
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Sequence 31 from Patent WO0246383.
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Matches:
Conservative:
Mismatches:
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                                  3.02e-72
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AK075142 2810 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90661 fis, clone PLACE1005003, weakly similar to PROSTASIN PRECURSOR (EC 3.4.21.-).

DEFINITION

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Logai, T. and Otsuki, T.

Direct Submission

Submitted (12-MRA-2002) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mall:genomics&hri.co.jb, Tel:81-438-52-3975, Fax:81-438-52-3986)

MEDO human cDNA sequencing project supported by Ministry of

Research Association for Biotechnology; cDNA full insert sequencing:

Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of

Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass

sequencing and clone selection: Helix Research Institute (supported
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                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_Tib="PlaCE1"
/note="Cloning vector: pME185FL3"
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AK075142.1 GI:22761040
oligo capping; fis (full insert sequence)
Homo sapiens (human)
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/note="unnamed protein product"
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Koga,H.

Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 650 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/650
PD 22-JAN-2002
PP 70-JUL-2000 JP 2000253172
PP 70-JUL-2000 JP 2000253172
PP 10-SHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI 158HI,
PI ISHII,
PI ISHII,
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1 (Dases 1 to 670)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Ota,T., Nishikawa,T., Nagai,T., Kojima,S., Otsuki,T. and
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full-length cDNA and use thereof
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BD125219 1 GI:23220164
JP 202017375-A/650
Homo sapiens (human)
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                             1.28e-44
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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rrrpProTrpGlnValSerLeuHisHisGlyGlyGlyGlyHisIleCysGlyGlySerLeuIl
                 eAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPr
                                                                                                 oAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAl
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Regulation of human prostasin-like serine protease Patent: WO 0198467-A 1 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Sequence 1 from Patent WO0198467.
AX342934
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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22-JAN-2002
07-JUL-2000 JP 2000253172
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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PD 22-JMN-2002
PD 12-UJL-2000 JP 200253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHJ
PI SHII,
YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
SHINICHI KOJIWA.
                                                    Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 1916 22-JAN-2002; HELIX RESEARCH INSTITUTE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of human prostasin-like serine protease
Patent: WO 0198467-A 3 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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                               197 GluleuArgLeuLeuGlyGlu-AlaThrCysGlnCysLeuTyr 210
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Mismatches:
Indels:
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Matches:

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                                                                                                                                                                    Sequence 3 from Patent WO0198467.
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AC009088/c
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AX342936/c
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Finishing Completed at Stanford Human Genome Center and Los Alamos
Finishing Completed at Stanford Human Genome Center and Los Alamos
Mational Laboratord.

Www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.

Estimated Total Number of Errors is 0.2.

Sequence is 233.4kb). It is clipped at the overlap with AC135050.

The number of bases overlapped is 2575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 127769)

DOE Joint Genome Institute.
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Submitted (03-APR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 127769)
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Direct Submission
                                                                                                                                                                                                                                                                               Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12774)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
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Unpublished
2 (bases 1 to 127769)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                  AC009088.9 GI:29366934
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716.50
50.81%
50.49%
36.69%
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FEATURES Location/Qualifiers source 11796 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Alignment Scores: 2.4e-29 Length: 1796 Pred. No.: 697.00 Marches: 160 Score: 65.29\$ Conservative: 49 Percent Similarity: 42.33\$ Mismatches: 133 Best Local Similarity: 35.69\$ Indels: 16 DB: 6	US-10-037-417-46 (1-357) x AX098193 (1-1796) QY	210 200 36	56 GlyThrTI 56 GlyThrTI 311 GGTCAGTC 76 LeulleA	Db 371 CICCIOINTESENVALLEULEUGIVALHISSENGINASPGIYPTOLEUASP 115 OY 96 GlubroalaalaGluTrpSerValLeuLeuGiyValHisSerGlnAspGlyProLeuAsp 115 ::	136 542 156 602	176 ThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGlu 19 	Oy 196 ValgluLeuArgleuLeudlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro 215
TGGTC	CGCCC 3190:	Db 31848 GGCATCATGGTTCCGAGTGGGGCAGCTGCGGACTGGTCCCACCCCCTCCATAT 51789 Qy 31788 CCGGGTCTGAATCCCATCTTTCCAATGACCCCCCCCCCC	31728	31608	125 EVALVAIDE CONTROL CONTRO	165 31368 185 31308		RESULT 12 AX098193 AX

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ITGGSSAVAGOWPMOVSITYEGVHÜCGGSLVSEÖWVLSAAHCFPSEHHKEAYEVKÜĞA
HQLDSYSEDAKVSTLKDIIPHPSYLQEGSGGJILLLQLSRFTTFSKYTRFICLLPAAN
FENDLIGTYTÜGMGHVAPRYEVSTLIFFSKYLQLEVPLISRETCNCLYIDAKPBEPHFVÜ
EDWYCAGYEGGEKDACÇGISGGELSCPVEGLIMYLTGIYSWGDACGARNREGGYTLASS
YASWIQSKVTELQPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLIRPILFIPLGLALG
                                                                                                                                                                                                                                                                                                                                                                                           clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: j Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MAQKGVLGPGQLGAVAILLYLGLLRSGTGAEGAEAPCGVAPQAR
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Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blatesley,R.W., Guoffard,G.G., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Logespi,R.,
Maduro,Q.L., Masklei,D.C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
Maduro,Q.L., Partson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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/note="Tryp SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:smaxt00020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetalaginiysgiyValLeuGlyProGlyGinLeuGlyAlaValAlaAsnSerAspSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Placenta, choriocarcinoma"
/clone lib="NHH MGC_21"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
product="prostasin preproprotein"
/protein_id="MAH01462.1"
/db_xref="GI:12655207"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:2133_IMAGE:3138532"
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Matches:
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/db_xref="LocusID:5652"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="LocusID:5652"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xref="MIM:600823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Best Local Similarity:
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Peingold, E.A., Grouse, L.H., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Wagner, L., Shemen, C.F., Bhat, N.K.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haish, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Garninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.J., Malek, J.A., Gunaratha, P.H., Richards, S.,
McKernan, K.J., Malek, J.A., Guaratha, P.H., Richards, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 04-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                           1076 CACCTGGCCTTCAGCTCTGCCCCAGCCTAGCTGAGGCCCATCCTTTCCTGCCT 1135
                                                                                                                                                                                                                                 1016 CAGCCTCGTGTGGTGCCCCAAACCCAGGAGTCCCAGCCCGACAGCAACCTCTGTGGCAGC 1075
                                                                                                            ----ACAGAÁCTC 1015
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                                                                                                                                                                                        CysLeuHis 312
                                     276 PheThralaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluPro 295
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                           313 GlnThrAlaPheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1136 CIGGGCCTGGCTCTGGGC-----CTCCTCTCCCCATGGCTCAGGGAGCACTGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12655206.
Contact: MGC help desk
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962 TACACTCTGGCCTCCAGCTAIGCCTCCTGGATCCAAAGCAAGGTG-
                                                                                                                                                                                           296 GlyProAlaPheProThrGlnProGlnLysThrGlnSerAsp-
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Tissue Procurement: ATCC
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JOURNAL
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KEYWORDS
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Pred. No.:
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                     LeulleAlaProSerTrpValleuSerAlaAlaHisCysPheMetThrAsnGlyThrLeu
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

linear

Sequence 6286 from Patent WO0194629. AX335777

AX335777

LOCUS DEFINITION

AX335777.1 GI:18126496

Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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CCTGAGGAGCCGCACTTTGTCCAAGAGACATGGTGTGTGCTGGCTAATGTGGAGGGGC 918
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Indels:
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Matches:
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/db_xref="taxon:9606"
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Patent: WO 0194629-A 6585 13-DEC-2001,
Avalon Pharmaceuticals (US)
Location/Qualifiers

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    /db_xref="taxon:9606"

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Human; NOVX; neurological disorder; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;

KW addiction; ardiovascular disease; hypertension; reproductive disorder;

KW autoimmune disease; and disease; hypertension; reproductive disorder;

KW pancreatitis; cirrhosis; glomerular endothelicisis; bacterial infection;

KW polycystic kidney disease; endorine disorder; obesity; cardiomyopathy;

KW polycystic kidney disease; andorine disorder; obesity; cardiomyopathy;

KW polycystic kidney disease; andorine disorder;

KW metabolic pathway regulation disorder; cytostatic; neuroprotective;

KW metabolic pathway regulation disorder; cytostatic; neuroprotective;

KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

KW definerological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

KW definerolisis; forensic biology; transgenic animal; drug screening;

KW gene therapy; NOV14a; prostatin precursor-like; chromosome 16; gene; ds.
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(CURA-) CURAGEN CORP.

Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;
Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;
Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;
Rochenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;
Padigaru M, Taupier RJ, Miller CE, Eisen A;

WPI; 2002-583619/62. P-PSDB; ABB09523.

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders.

Claim 9a; Page 142; 323pp; English.

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (AB093092). NOVX proteins and nucleic acids encoding them (AB093092). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX cassociated disorders or in the manufacture of a medicament for treating associated disorders or in the manufacture of a medicament for treating cassociated disorders or in the manufacture of a medicament for treating cassociated with Sports of a medicament for treating cassociated with Sports of them of the 24 cassociated with Sports of sold medicament for the 24 cassociated with NOVX proteins including neurological disorders (e.g., Alzheimer's Huntington's and parkinson's diseases), cash, behavioural disorders, addiction, tuberous sclerosis, cancers of e.g., allergies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., phypertension), reproductive disorates, endometriosis, incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, circontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, diabetes, circontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disporters, polycystic kidney diseases, endocreations, incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disporters, or incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disporters, or incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disporters, or incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disporters, or incontinence, psoriasis, scleroderma, alopecia, obesity, bacterial infections and particularly dates or downstream effectors which as neurogenesis, cell differentiation. NOVX nucleic acids sequences can be used to identify a cell or tissue type and comprising NOVX nucleication of identifying and cloning NOVX homologues in other cell types ore

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The invention relates to 24 novel human proteins designated NOVI-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABE098879-ABE09302). NOVX proteins and nucleic acids encoding them (ABE098879-ABE09302). NOVX proteins and nucleic acids encoding them (ABE098879-ABE09302). NOVX proteins and associated disorders or in the manufacture of a medicament for treating associated disorders or in the manufacture of a medicament for treating such disorders with specific applications described for each of the 24 NOVX proteins, based on their homology to known proteins. Various disorders (e.g., Albraimer's 's' Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tuberous sclerosis, cancers (e.g., allergies and autoimmune disorders, myasthenia gravis, asthma, various forms of arthritis diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, cardiomypathy, cincontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, cinchosis, glomerular endotheliosis, polycystic kidney disease, endocrine corrinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disorders, obesity, bacterial infections and parkinalarly cardiomypathy, disorders, obesity, bacterial infections and parkinalarly cardiomypathy, be used to identify callular receptors or downstream effectors which be used to identify and are also useful as targets for the correspication, haematopoiesis, wound healing and angiogenesis. Correspication, haematopoiesis, wound healing and angiogenesis or inclication as a source of primers or probes for forensic biology and for are useful as a source of primers or probes for forensic biology and comprising NOVX mucleic acids are useful for producing non-inman and enimals which are useful deviating and evaluating modulators of nover an animals which are useful deviating and evaluating modulators of nover inferiors and for identifying and evaluating and evaluating modulators of NOVX proteins an
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                             Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune
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28-FEB-2001; 2001US-0272411P.
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Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders (e.g. restenosis) and inflammatory

Claim 26; Fig 1SS-TT; 313pp; English.

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Sudarsanam S, Manning G,

Whyte D,

Charydczak G;

Plowman G,

(SUGE-) SUGEN INC

WPI; 2002-139913/18. P-PSDB; AAU82753.

26-JUN-2001; 2001WO-US020171 26-JUN-2000; 2000US-0214047P

03-JAN-2002.

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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are cand the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lumgy, immune-related diseases and disorders (e.g. infilammatory diseases at asthmal, cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. disorders, pain, sexual dysfunction, mood disorders, attention cdiseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, confiling disorders, hypertension, psychotic disorders, neurological disorders, hypertension, pypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency cure liffy, and non-viral infections such as ocular disease (e.g. sequences encoding for the novel human procteases of the invention
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Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; gene; ds.

WO200200860-A2 Homo sapiens.

DNA encoding novel human protease #52.

23-APR-2002 (first entry)

BP

standard; DNA; 2457

ABK31795 ABK31795;

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Azimzai Y, Kallick DA, Baughn MR, Griffin JA, Swarnakar A;
Walia NK, Hafalia AJA, Gandhi AR, Au-Young J, Elliott VS;
r J, Thangavelu K, Iu Y, Warren BA, Iu DAM, Lee EA;
ey CM, Arvizu C, Delegeane AM, Yao MG, Khan FA;
        08-DEC-2000; 2000US-0254399P.
21-DEC-2000; 2000US-0257803P.
05-JAN-2001; 2001US-0260110P.
19-JAN-2001; 2001US-026851P.
25-JAN-2001; 2001US-0264623P.
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A mitianaemic; antiinflammatory; antiidiabetic; antippretic; virucide;

A mitianacemic; osteopathic; antiemetic; antipyretic; virucide;

A mitianaceria; fungicide; gastrointestinal; antidiarrheic; laxative;

A mitianaceria; anti-HIV; thrombolytic; anticoagulant; gynaecological;

A manitumour; antiarteriosolerotic; hypotensive; vasotropic;

A mitianumui; antintemmatic; immunosuppressive; antiallergic; antithyroid;

W antitumour; antistermedic; immunosuppressive; antiallergic; antithyroid;

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M nophrotropic; antiqous; thyromimetic; antialergic; antimfertility;

M nophralmological; antidepressant; neuroleptic; antimfertility;

M auditory; antiseborrheic; antidepressant; neuroleptic; antimfertility;

M nophralmological; antidepressant; neuroleptic; antimfertility;

M nophralmological; Alzheimer's disease; hypertension; autoimmune;

M scabies; neurological; Alzheimer's disease; reproductive;

W ectopic pregnancy; gene therapy; vaccine; disorder; prostasin; gene; ss.
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                                                                                                                                 The invention relates to an isolated Protein Modification and Maintenance (PPMM) polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. anaemia), rell hypertension), autoimmune/inflammatory disorders (e.g. anaemia), cell proliferative disorders, developmental disorders (e.g. anaemia), rell exproductive disorders (e.g. Alzheimer's disease) (e.g. scabise), meurological disorders (e.g. Alzheimer's disease) exproductive disorders (e.g. actopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the aspessment of the effects of exogenous compound on the expression of nucleic assessment of the expression of machine mains and amino and amino and active pression and and amino and active diseases.
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New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.
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K, Kojima S, Ots
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02-MAY-2000; 2000JP-00183765.
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and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length CDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to modulate enzyme activity in a disease, such as metastable of malignant cells, tumour angiogenesis, inflammation, chronic obstructive malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease (e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease gene provides a therapeutic target of decreasing human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic,
                                                                                                                                                                                                                                                             Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; aherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-dakob disease; metastatic cancer; lipid accumulation; osteoprosis; Paget's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention comprises the CDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypasin-like serine protease purified from human seminal fluid. An antibody specific for prostasin-like serine protease is useful for immundetection and diagnosis of micro-metastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be
 863 IGCIGIGGCIACCIAIGAGGCAIGGAIACGGGAGCAGGIGAIGGGIICAGAGCCIGGGCC 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'partial
'note= "No start or stop codons shown"
                                    oAlaPheProThrGlnProGlnLysThrGlnSerAsp 309
                                                         'product= "Prostasin-like enzyme"
                                                                                                                                                                                                                                    Human prostasin-like serine protease cDNA #1
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20-MAR-2001; 2001US-0276909P.
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augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like berine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #1 nucleotide sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 537 BP; 92 A; 176 C; 197 G; 72 T; 0 U; 0 Other;
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us-10-037-417-46.p2n.rng

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The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA illength clones were obtained by construction of full length enriched cDNA illength clones were synthesised by the oligo-capping method. The primers libraries that were synthesised by the oligo-capping method. The primers methods. The present sequence was used as the representative sequence from a human clone which was used in howology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for synthesizing full length cDNA clones and their use
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                                                            503 TGTCTGCCTGCCCCGCGCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGGGCCACCGG
                                  177 yTrpGlyAspVal-GlnGluAlaAspProLeuProLeuProTrpValLeuGln-GluVal
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                  Human cDNA clone representative sequence, SEQ ID NO: 1916.
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                                                                                                                                     623 GAGCTAAGGNTGCTGGCGAAGGCAACTGGTCAATGTCTCTAC 665
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Conservative:
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K, Kojima
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su A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Best Local Similarity:
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Pred. No.:
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T, Koga
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3, Otsuki
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K, Kojima S
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A T, Nagai
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Novel human prostasin-like serine protease polypeptide and polynucleotide
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                                          rTrpProTrpGlnValSerLeuHisHisGlyGlyHisIleCysGlyGlyGrLeuIl
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20-MAR-2001; 2001US-0276909P.
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ID ABK13566 standard; cDNA; 456
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Alignment Scores:

Pred. No.:

Scores:

199.00

Matches:

147

799.00

Conservative:

Percent Similarity:

96.71$

Mismatches:

4

Chery Match:

6.91$

Gaps:

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US-10-037-417-46 (1-357) x ABK13566 (1-456)

λά	97 ProAla	97 ProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGly 116
qa	456 CCCGCG	ccececeaeceargeargearacatacaecentecactecaaeaaceecergeaceec 397
ò	117 AlaHis	AlaHisThrArgAlaValAlaAlaIleValValValProAlaAsnTyrSerGlnValGluLeu 136
· q	396 GCGCAC	GCGCACACCGCNGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTG 337
ò	137 GlyAla	GlyalaaspLeualaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrp 156
: 8	336 GGCGCC	336 GGCCCGACCTGCCCTGCTCGCCTCACCCGCCAGCCTGGGCCCCGCCGTGTGTGT
ò	157 ProVal	ProvalCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThr 176
: <u>4</u> 2	 276 CCTGTC	CTGTCTGCCTGCCTGCGCCTCACACCGCTTGCTGCACGGCACCGCCTGCTGGCCACC
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qq	96 AACCTC	

237 AspThrCysGlnGlyAspSerGlyGlyProLeuVal 248

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cannot be a states involving expressed capacity, of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cusful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging complement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders in diagnostics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and confidence the state of the sequences have applications or binding capacity and only applications of dequences have applications for assess biodiversity and to produce other types of data and products dependent on DNA and and an adaptosed the sequences have applications of mutations and equences have applications when the sequences have applications of mutations are applications. The sequence have a sesses biodiversity and to produce other types of data and products dependent on DNA and and an adaptoration when the sequences have a sequence to the sequences have a sequence of mutations and applications when the sequences have a sequence of the sequences have a sequence of mutations and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #4844.
36 GACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTC 1
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                                                                                                                                    ВЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167
                                                                                                                                    AAS69040 standard; cDNA; 597
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                                                                                                                                                                                                                                    (first entry)
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P-PSDB; ABG04853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2
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                                                                                                                                                                                       AAS69040;
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2e-35 787.50 94.41% 93.17%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Gaps:

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232
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                                                                          172 aCysTrpAlaThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpVa
                                                                                                                                                                                                          243 CIGCIGGECACCGCTGGGGAAACGICCAGGAGGCAGAICCICTCTGCCTCTCCCCTGGGT
                                                                                                                                                                                                                                 192 lLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGl
                                                                                                                                                                                                                                                   363 eccedencerreacereactereseanarreceaegarectereresecrace
                                                                                                                                                                                                                                                                                                                    ogluglyArgArgArgAspThrCysGln---GlyAspSerGlyGlyProLeuValCysGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the presence of breast cancer in an individual, involves using specific polynucleotide markers.
                                                           112 yProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValValProAlaAsnTyrSe
                                                                                                                                             152 yProAlaValTrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAl
                  GlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyVal-HisSerGluAspGl
                             rGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cancer / ovarian cancer related coding sequence #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; ds; cytostatic; breast cancer; ovarian cancer.
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US-10-037-417-46 (1-357) x AAS69040 (1-597)
                                                                                                                                                                                                                                                                                                                                                                                                                                ABT31936 standard; DNA; 1733 BP.
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27-JUN-2001; 2001US-0301351P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2002; 2002WO-US019773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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The invention comprises a method for assessing whether a patient is afflicted with breast cancer or ovarian cancer. The method involves the
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8888	afflicted use of speed detection ABT31894	wit.	h breast cancer o ic DNA markers. T treatment of ova T31949 encode hum	មិថ្មីអ៊ីធ្វី	ovarian e method ian and b n breast/	cancer of the reast ovaria		The method invention is ancer. DNA s	no no mi	-н ш	the in the eins	
X X	Sequence 1	1733 BP;	311 A; 5	78 C;	500 G;	344 T;	0 0;	0 Other	er;			
Aligi Pred Score Perce Best Query	Alignment Score: Pred. No.: Score: Percent Similar: Bet Local Similar Query Match: DB:	es: rity: ilarity:	5.65e-3 697.00 55.29% 42.33% 35.69%	0	Lengtl Match Conse Misma Indel Gaps:	h: es: rvative tches: s:	177 164 133 141					
US-10	0-037-417-4	46 (1-357	7) x ABT3	1936 (1-1733	_						
Š	т.	MetAlaGlr	aGlnLysGlyValLeuGlyProGlyGlnLe	llllll	yProGl	yGlnLeuGly	lyAla	ValAl	AsnS	erAspSe	er 20	
QQ	1 66	- D - D	GAAGGGGG	rccrada	GCCTGG	secaderies.	GGGGGCT	creresc	 O	1	14	y
Š	Н	TyrSerLe	euTyrG]	GlyLeuVa	ieuValProSe :::	TyrSerLeuTyrGlyLeuValProSerGlyProAlaArgGlyP		1 0	-Alahr	aArgGlyPr	ro 35	
qq	147 1	ATTCTGCT	CTATCTTG	BATTACT	CCGGT(agggacag	GAGCG	GAAGG	GGCAGA	AGCILC	מ ככ	۵
ολ	36	ProTyrCy:	sGlyAr	roGluPr	oSerA]	sGlyArgProGluProSerAlaArgIleVal	alGly(G1yse 	erAsnAla	원	55	
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QQ	258	dercagie	decended	AGGTCAG	CATCAC	CTATGAAG	ĠĊĠŦĊ	cargr	GTGTG	TGGCT	31	7
ζ	96	LeuileAl	aProSerT:	rpvalle	uSerA	LeuileAlaProSerTrpValieuSerAlaAlaHisCysPh	ysPhe	MetTh	PheMetThrAsnGlyThrL	yThru	6 7 6	
QQ	318	стсететс	TGAGCAGT	GGGTGCI	GTCAG	CTGCTCACT	GCTTC	CCCAG	CCCCAGCGAGCACCACAAG	ACCACA	m	7
δλ	96	ProAl	aAla	rpSerVa	lleur.	aGluTrpSerValLeuLeuGlyValHi	isser	GlnAs	sSerGlnAspGlyP1	roLeuA	Н	
Dp	378	GAA	GCCİ	ATGAGGI	CAAGC	gcciatgaggttgagcttgagcccaccaccagccagcccacc	ACCAC	SCTAGA	ĊTCCT?	ACTCCGAG	AG 42	89
à	116	GlyAlaHi	aHisThrArgAlaValAl	laValAl	aAlai	levalvalProAl	roAl	aAsnTy	yrSerGlnV	InvalG	Glu 13	Ŋ
ορ	429	GACGCCAA	GGTCAGCA	CCCTGA	GGACA	deargetergeacceterageacateatecececaceceagetaceeceages	ACCC(PAGCTA	άσπας	ĄĠĠĄĠĠ	3GC 48	
ζ	136	LeuGlyAl	aAspLeuAl	laLeuLe	uArgL	euArgLeuAlaSerProAla	roAl	SerLe	aSerLeuGlyProAl	roAlaVa :	T :	
qq	489	TCCCAGGG	ccacarre	cacreci	CCAAC	TCCCAGGGCĠĀĊATTĠĊĀĊŢĊĊŢĊCAĀĊŢĊAGCAGĀĊĊCATCACCTTCTCCGGCTĀCĀT	CCAT	CACCTI	יכדכככ	GCTACA	ώ υ	ω
δλ	156	TrpProVal	1CysLeuP	roArgAl	laSerHisAr :::	TrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAl(alHi:	gPheValHisGlyThrAl	rAlaCyB?	ysTrpAL	Ala 17	2
qq	549	CGGCCCAI	rerecerce	CTGCAG	CAACG	ccrcciric	CCAA	:GGCC:	rccacti	GĊACTG	3TC 60	œ
δ	176	ThrGlyTr	hrGlyTrpGlyAspV	alGlnGluAl	luAlaA	aAspProLeuE	role	uProTi	euProLeuProTrpValL	euglngl	31u 19	
qq	609	Acredere	SGGÍCATÓ	rideccc.	ccrcae	<u>actidecticidedicarididececeercagraaccificergaegeceaagecageagea</u>	TGAC	3CCCP/	AGCCAC	TĠĊĂĠĊ	y	
Š	196	ValGluLe	euArgLeuI	euGlyG	luAlaT 	alGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyP :: ::: :::	ysle	uTyrSe	erGlnP	roGlyE	0	
qq	699		recercies	TCAGTC	stgaga	rcandrigecticharcarcargagacacararachacharcarararaga	racci	GTACA	ACATCG	ACGCC	AG 7	28
à	216	PheAsnLe	PheAsnLeuThrLeuGl	lnileL	euProG	heAsnLeuThrLeuGlnIleLeuProGlyMetLeuCyaAlaGlyTyrProGluGlyArg	CYBAL	aGlyT)	yrProG	1uG1y	N	35
qq	729	CCTGAGG	AGCCGCACI	rtgrcc	AAGAGG	acardere	rgrac	TGGCT	Argred	AGGGGG	7	88
ò	236		hrCysGln(SlyAspS	erGly6	ArgAspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGly:::	ValCy	eGluG	OLEUVAlCyBGluGluGlyGlyArgTrp	lyArg	N	
qq	789		ccreccae	scrcacr	CTGGG	GCCCACTC	rccre	CCCTG	TGGAGG	E E	œ C	
δλ	256		laGlyIle:	ThrSerP	hedlyE	PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyVa	GlyAr 	garga 	snArgF 		7 7	
qq	849		ceádcatr	STGAĞÜT	GGGGAC	мтвсстет	GGGGC	CCGCA	ACAGGC	CTGGT	හ ආ	80

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The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see AAF98594 to AAF98730), in a patient sample, and (2) the mornal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have expositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated for: (1) assessing and treating ovarian cancer; (2) making isolated assessment, and (3) inhibiting ovarian cancer in a patient. AAF988573 to AAF988593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
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                  -----ÇyşLeuHis 312
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276 PheThralaValAlaThrTyrGluAlaTrpileArgGluGlnValMetGlySerGluPro
                                                                                                                                                                                                              1083 CIGGGCCTGGCTCTGGGC------CTCCTCTCCCCAIGGCTCAGCAAGCACTGAGCT
                                                                                                                          313 GlnThrAlaPheLeuAspSer---AlaArglleLeuLeuArgProLeuSerHisIleSer
                                                                                                                                                                                                                                                                                 1134 GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACGAGGAGGCTGGTCCTTC 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovarian cancer; identification; detection; characterisation; kinase; marker; cytostatic; antisense gene therapy; ds.
                                                                                                                                                                                                                                                        -----ProHisSerLeuLeuGlyLeuTrpGlyPhe 357
                                                                                                                                                                                          332 ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer
                                                               296 GlyProAlaPheProThrGlnProGlnLysThrGlnSerAsp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ovarian cancer cell expressed sequence 10798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1001-1002; 1198pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAF98698 standard; DNA; 1796 BP.
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21-MAR-2000; 2000US-0191321P.
31-MAY-2000; 2000US-0208382P.
20-JUL-2000; 2000US-00220467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
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The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of
1016 CAGCCTCGTGTGCCCCCAAACCCAGGAGTCCCAGCCGACACCTCTGTGGCAGC 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                           GlnThrAlaPheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer
                                                                                                                 1076 CACCTGGCCTTCAGCTCTGCCCCAGGCCTTGCTGAGGCCCATCTTTCCTGCCT
                                                                                                                                                                                                                        GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACGAGGAGCCTGGTCCTTC 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                                                                                                                                                                                         ---ProHisSerLeuLeuGlyLeuTrpGlyPhe
                                                                                                                                                                                     ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding human ovarian cancer marker OV80.
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2001US-0311732P.
2001US-0323580P.
2001US-0324967P.
2001US-0325102P.
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19-SEP-2001;
26-SEP-2001;
26-SEP-2001;
26-SEP-2001;
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                0 U; 0 Other;
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160
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133
36
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Matches:
Conservative:
Mismatches:
Indels:
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                     G; 359 T;
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                     327 A; 599
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                     Sequence 1796 BP;
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Best Local Similarity:
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covarian cancer (e.g. patients having an enhanced risk of developing covarian cancer (e.g. patients having a familial history of ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and calsorders (e.g. cerebral cedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), connective tissue disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atheroscalerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with covarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastrasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the convarian carcinogenic potential of a compound, or inhibiting ovarian cancer cancer at risk of developing ovarian cancer. The present nucleic acide in the convarian cancer markers described in the
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U; 0 Other; T; 0 Sequence 1834 BP; 309 A; 621 C; 526 G; 378

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799 CTCGAGGTGCCTCTGATCAGTCGTGAGACGTGAACTGCCTGTACAACATCGACGCCAAG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                       1153 CACCTGGCCTTCAGCTCTGCCCCAGGCCTTGTTGCTGAGGCCCATCCTTTTCCTGCCT
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Soppet DR,
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Horrigan S;

Endress G,

Ebner R,

000US-0237425P

000US-0237606P

The present invention describes a method (M1) for screening for an antic neoplastic agent. The method involves exposing cells to a chemical agent
c neoplastic agent. The method involves exposing cells to a chemical agent
c to be tested for anti-neoplastic activity, determining a change in
c expression of at least one gene (I) of a signature gene set, where (I)
c comprises a sequence (S) selected from 8447 sequences (given in ABL61664
c c ABL70110), or is at least 95% identical to (S), where a change in
c expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening an
c anti-neoplastic agent, and can be used for producing a product which is
che data collected with respect to the anti-neoplastic agent as a result
of M1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney,
c prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set. Claim 1; SEQ ID NO 6286; 44pp; English Carter KC, Augustus M, Weaver Z; (AVAL-) AVALON PHARM. WPI; 2002-188264/24.

Sequence 1834 BP; 309 A; 621 C; 526 G; 378 T; 0 U; 0 Other;

> Length:
> Matches:
> Conservative:
> Mismatches:
> Indels: 5.97e-30 697.00 55.29% 42.33% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores:

US-10-037-417-46 (1-357) x ABL67949 (1-1834)

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δy	36 ProTyrCysGlyArgProGluProSerAlaArg1leValGlyGlySerAsnAlaGlnPro 5:	Ŋ
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<u></u>	508 GAAGCCTAIGAGGTCAAGGGGCCCACCAGCTAGAGACTCCTACTCGAG 5	
λō	Ęř	35
ΩÞ	559 GACGCCAAGGTCAGCACCCTGAAGGACATCCACCCCACC	18
Š	136 LeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaVal 1	55
Db	619 receaggadatideachechecacheagagaeceareacherecegeracare 6	78
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Dp	679 cggcccarchdccrccacaccaccaccrccrrccaaacgccrccacrgcacrgrc 7	m
È	6 ThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGlu	6
qq	739 ACTGGCTGGGGTCATGTGGCCCCCTCAGTGAGCCTCCTGACGCCCAAGCCACTGCAGCAA 7	σ.
ζŎ	196 ValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro 2 ::: ::: :::	H
Db		D.
δχ	216 PheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArg 2	m
Db		918
δ	236 ArgAspThrCysGlnGlyAspSerGlyGlyProbeuValCysGluGluGlyGlyArgTrp 2	52
q 0		978
δ	256 PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyVal 3	275
ΩÞ		1038
ò	276 PheThrAlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluPro	295
QQ	7.3	1092
Qy	296 GlyProAlaPheProThrGlnProGlnLysThrGlnSerAspCysLeuHis	312
qa	r)	1152
ò	313 GlnThrAlaPheLeuAspSerAlaArglleLeuLeuArgProLeuSerHislleSer	331
qq		1212
Š	332 ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer	47
qq	checrecedardecreadeageacreager	1263
à	348	
qq	1264 GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACAGGAGCCTGGTCCTTC 1317	

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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an activity and can be used for producing a product which is anti-neoplastic agent, and can be used for producing a product which is compreted with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcer, squamous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAsp 115
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeulleAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaGlnLysGlyValLeuGlyProGlyGlnLeuGlyAlaValAlaAsnSerAspSer
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                                                                                     Claim 1; SEQ ID NO 6849; 44pp; English
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Weaver Z;
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               RESULT 15
ABL68512
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447

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1039 TACACTCTGGCCTCCAGCTATGCCTCCTGGATCCAAAGGAGGTG-----ACAGAACTC 1092
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196 ValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro 215
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Search completed: February 25, 2004, 16:16:14 Job time : 429 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on:

February 25, 2004, 15:57:04; Search time 2489 Seconds (without alignments) 4283.165 Million cell updates/sec US-10-037-417-46 1953 1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357 Perfect score: Scoring table: Sequence: Title:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62

27513289 segs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=x1p
-MODEL=frame+_p2n.model -DEV=x1p
-Q=/cogn_2 1/USFPTO spool p/USION37417/runat_24022004_101038_17460/app_query.fasta_1.519
-DEST_OFWT=fastap -SUFFIX=p2n.rst -MINNATCH=0.1 -LOCPCL=0 -LOCPEXT=0
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-USER=USI0037417 @CGN 1_1 3549 @runat_2402204_101038_17460 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN T-NSPBLCCK=100 -TONGLOG
-DEV_TIMEOUT=120 -WARN T-NSPBLCCK=100 -TONGLOG
-PGAPEXT=7 -YGAPOP=10 -YGAPDEXT=0.5 -DELDEXT=7

EST:* Database

1: em_estba:.*
2: em_estbum:.*
4: em_estin:.*
5: em_estpl:.*
7: em_estpl:.*
7: em_estpl:.*
10: gb_est2:.*
11: gb_htc:*

gb_est4:* gb_est5:* gb_est3:*

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em_gss_vrt:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	iption	AW450407 UI-H-BI3-	509 ad49£	3696 Mus	0640 Mus	170 A	660 BX8	181 Mus musc	m	81	294	CF238383 AGENCOURT	192		326	BO729181 AGENCOURT		AK014645 Mus muscu	3 5	ALS/8261 ALS/8261	BOYZZY64 AGENCOUKI	BX///626 BX///626	CFISIUS/ AGENCOURI	sn.	au.	AK052738 Mus muscu	GENCOU	BY710051 BY710051	AL555870 AL555870	BM923713 AGENCOURT	CK029454 AGENCOURT	٦ <u>١</u>	0 -	BI218460 602937954	33	3558	22	5	62187	42120	1192	00011 AGENCOUR	9117 602835	508404 CDA90-F1	2972	
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ALIGNMENTS

UI-HOLY. Innear EST 17-FEB-2000 UI-H BEI3-akn-g-11-0-UI.81 NCI_CGAP_Sub5 Homo sapiens CDNA clone INAGE:2735037 3', mRNA sequence. AW450407.1 GI:6991183 RESULT 1 AW450407/c LOCUS DEFINITION ACCESSION

VERSION KEYWORDS

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537) EST. Homo sapiens (human) Homo sapiens SOURCE ORGANISM

REFERENCE

357

175

237

297

215

57

AUTHORS JOURNAL

COMMENT

source

FEATURES

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AI190509 456 bp mRNA linear EST 28-OCT-1998 qd49f07.x1 Soares fetal heart NDHH19W Homo sapiens cDNA clone IMAGE:1732837 3' Similar to SW:MCP6_MOUSE P21845 MAST CELL PROTEASE 6 PRECURSOR;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 ACCGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCCTCTCCCCTGGGTGCTACAGGAA 177
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 456)
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Email: cgapbs-remmal..nih.gov
This clone is available royalty-free through LiNL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
INSECT Consortium (info@image.linl.gov) for further information.
Seq primer: -400P from Gabco
High quality sequence stop: 452.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                        196 ValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro
                                                                                                GlyAlaHisThrArgAlaValAlaAlaIleValValValProAlaAsnTyrSerGlnValGlu
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1414920-14178412-1203044-122439); NCI CGAP GC4 pool 1 LIAM
3164-3167, 3716-3720, 3733-3735 (IRAGE CloneIDS
1227096-1258611,1465064-1470983, 1475282-1476743);
NCI CGAP Pr22 pool 1 LIAM 2457-2459, 2758-2759, 3062-3068
(IRAGE CLOREIDS 985608-986759,1001122-1101959,
1217928-1220615); NCI CGAP COLO pool 1 LIAM 2644-2653,
2871-2872 (IRAGE CLOREIDS 2708616-2710535) and
NCI CGAP Sub1 (IRAGE CLOREIDS 2708616-2710535) and
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NCI CGAP Sub2 (IRAGE CLOREIDS 2708616-2710535) and
NCI CGAP Sub2 (IRAGE CLOREIDS 2708616-2710535) and
NCI CGAP Sub2 (IRAGE CLOREIDS 2708536-272455) (10% of the driver population), plus a pool of 11,136 clones from
NCI CGAP Sub2 (IRAGE CLOREIDS 2712455-272455) (10% of the driver population), plus a pool of 5,472 clones from
CCCGAP Pub4 (IRAGE CLOREIDS 2712455-2722891) (10% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Recalitate Gene Discovery. Genome Research 6, 791-806.
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/clone lib="NGI CGAP Sub5" |
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                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Oligo-dr track not found, Not site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
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             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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TAG_SEQ=AAACG"
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 1699)

Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Puruno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Puruno,M., Haranco,K., Hiroka,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Niyazaki,A., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,K., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagawi,M., Takada,Y., Takaku-Akahira,S., Takaku-Akahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku,M., Tomara,M., Toya,T., Yasunishi,A., Thiraka,T., Takaku-Kahira,S., Takaku,M., Tomara,M., Toya,T., Yasunishi,A., Thiraka,T., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takaku-Kahira,S., Takahira,S., Takahanira,S., Takahanira,S., Takaku-Kahira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahanira,S., Takahira,S., 
                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Rashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Tzawa, M., Ohara, E., Watshika, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), 'Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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/db_xref="MGI:2396949"
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URL:http://fantom.gec.riken.go.jp/
Location/Qualifiers
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/clone="7530415E19"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCGGGCCGACTGGTGGTGCTGTGGGGCGNTGCACTCCAAGGACGGCCCCTGGACGGC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGluLeu 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 CCTGTCTGCCTGCCCGCGCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGGGCACC 217
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 GCGCACACCCCNGCAGTGGCCGCCATCGTGCTGCCGGCCAACTACAGCCAAGTGGAGCTG
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Matches:
Conservative:
Mismatches:
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mus musculus (house mouse)
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Best Local Similarity:
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AK078696
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AK010640 1629 bp mRNA linear HTC 20-SEP-2003
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410039E18 product:PROSTASIN, full insert sequence.
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                                                                                                                                                                                                                                                                                                                1054 CCTCGAGTTGTCCCCCAGACTCAGGAGTCCCAGCCGGATGGCCACCTCTGCAACCATCAT 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, T., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsundo, H., Sakaguchi, S., Ikegami, T., Kashiwadi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                  940 TIGGCAGGCATIGTGAGTITGTGAGGTGATGCCTGTGGTGCCCCCAACAGGCCTGGAGTATAC 999
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237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPhe
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Mature 420, 563-573 (2002)

S Adachi, U., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatau, N., Hiramoto, K., Haraoka, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kosukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Nomura, K., Numazaki, R., Ohno, M., Okazaki, A., Nishi, K., Saito, H., Saito, R., Sakai, C., Saaito, H., Sasaki, D., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Yanamara, Y., Yanamara, Y., Yanamara, Y., Yanamara, Y., Yanamara, Y., Yanamara, Y., Yanamara, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yana, Yan
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Mismatches:
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EST 31-MAY-2003

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RZPDLIB; I.M.A.G.B. CDNA Clone Collection (amp- resistant) (RZPDLIB No.998) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus laevis Unidene Set I (RZPDLIB No.988) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX844660 MICHD XGC Emb4 Xenopus laevis cDNA clone IMAGp998C059551; IMAGE:4203196 5', mRNA sequence.
                                                                                                                                                                                                                                                                              156 TrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 GlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGlu 135
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
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                                                                                                                                                                                            538 TCCCAGGGGGACATTGCACTCCTCCCAACTCAGCAGACCCATCACCTTCTCCCGCTACATC
                                                                                                                                                                                                                                                                                                                                        598 ceccicarcrecircorrecadocaacecerecirioeceaacedecereardedacerere
                                                                                                                                                                                                                                                                                                                                                                                                      176 ThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGlu
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                                                                          478 GACGCCAAGGTCAGCACCCTGAAGGACATCATCCCCCACCCCAGCTACCTCCAGGAGGGC
                                                                                                                                                        136 LeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 ArgAspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrp
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1 (bases 1 to 911)

Reli(O., Neubert, P., Peters, M., Radelof, U., Schneider, D., Schroth, A., Korr, B. and Landgrebe, J.

Xenopus laevis UniGene Set 1 (RZPDLIB No.988)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Ilm Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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   sapiens cDNA
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                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1071)
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7896.r For
more information about this cluster, see
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AL551470 Homo sapiens PLACENTA COT 25-NORMALIZED Homo
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On Feb 15, 2001 this sequence version replaced
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                                                                                    AL551470.2 GI:31273286
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Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630023F11 product:similar to MARAPSIN PRECURSOR (EC 3.4.21.-) [Homo sapiens], full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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                                                                                                                             SerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThrAlaValAlaThr 281
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
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Gasterosteus aculeatus
Gasterosteus aculeatus
Gasterosteus (Hordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
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LEGEWPWQVSIQRNGIHFCGGSLIAPTWVLTAAHCFSNTSDISIYQVLLGALKLQQPG
PHALYVPVKQVKSNPQYQGMASSADVALVELQGPVTFTNYILPVCLPDPSVIFESGMN
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  Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Muramatsu,M. and Hayashizaki,Y.

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (R-mail:genome-res@gsc.riken.go.jp, DKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                              CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wallcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.
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/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; putative
similar to MARAPSIN PRECURSOR (EC 3.4.21.-) [Homo sapiens]
(SWISSPROT|Q9BQR3, evidence: FASTY, 76.5%ID, 100%length,
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/db_xref="MGI:2406613"
/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="G1:26348449"
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hab64c07, yl Fugu UT7 adult skin Takifugu rubripes cDNA clone
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Email: zbrafish@watson.wustl.edu
Libzary materials provided by G. Elgar (UK MRC HGMP-RC) Library
constructed by Drs. K. Kakami, M. Sasaki, S. Sugano, K. Kikuchi
and S. Watabe (University of Tokyo, Institute of Medical Science
and Laboratory of Aquatic Molecular Biology and Biotechnology) DNA
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                         Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
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                         1 (bases 1 to 1044)
Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M.,
Schmutz,J. and Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCACTGCTTCTCCCAGCACCAGT------CCTTCCGGTCTCACCGTGTACCTC 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="mixed male and female"
/tissue_type="heads and internal organs combined"
                                                                                                                   Expressed sequence tags from Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1044
120
32
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26
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Salinas river, CA"
                                                                                                                                                                                                                                                                                   Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 793.
Location/Qualifiers
1. .1044
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Gasterosteidae; Gasterosteus.
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Best Local Similarity:
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L (Dases 1 to 1189)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Feingold, E.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bondloo, W.F., Casavanth, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McKwan, P.J.,
McKernan, K.J., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Manzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, W., Wadan, A., Young, A.C., Shevchenko, Y.,
Buckeria, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Sochein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse odna Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC034294 1188 bp mRNA linear HTC 17-DEC-2003
Homo sapiens cDNA clone IMAGE:4752547, containing frame-shift
                                                                                                                                                                                                                                                                                                                                                           258 AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr 277
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1188)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                        ThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPheGln
                                                                                                                                                                                                                                                                  ---GTGGGAAGGATAACGGACAACATGGTCTGTGCCGGGGTTGCGCAGGGGGGAAGAT
                                                                         218 LeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAgp
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Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM.HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 AlavalAlaThrTyrGluAlaTrpileArgGluGlnVal 290
562 GIGCCCAICAGGGGAACAGGGAGIGIAACIGIAACIACGGA-
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Contact: MGC help desk
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Homo sapiens
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Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /issue_type="skin"
/lab_host="DH10B (T1 phage-resistant)"
/cloon=lib="Hogu UT7 adult skin"
/cloon=lib="Hogu UT7 adult skin"
/cloot="Vector: pBluescript-FL; Site 1: PflM I
/cCANNNNTGG); Site 2: PflM I (CCANNNNTGG); BamHI-Smal
sites were converted to BamHI-FILMI-Sfil-FflIM sites (Smal
is destroyed). Other part of the vector is untouched. The
cDNA is inserted between two PflMI sites in T3 (5') to T7
(3') direction. Library materials provided by G. Elgar (UK
MRC HEGRP-RC) and constructed and donated by Drs. K.
Kawakami, M. Sasaki, S. Sugano, K. Kikuchi and S. Watabe
(University of Tokyo, Institute of Medical Science and
Sequencing by: Washington University Genome Sequencing Center Clone distribution: Fugu clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: info@image.llnl.gov
Seq primer: T3 ET from Amersham
High quality sequence stop: 490.
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Matches:
Conservative:
Mismatches:
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|clone="IMAGE:6353269"
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/doing="Image:693385"
/tissue_type="neurula"
/dev stage="embryo.stages 14-19"
/lab_host="DHIDB (phage=resistant)"
/clone_lib="NHICHD XGC_Emb6"
/note="Vector: pCWV-SPORT6.1, Site_1: Not1; Site_2: ECORV;
Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 05-AUG-2003
                                                                                                                                                                                                                  --ThralaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGly 292
                                                                                                                                                                                                                                                                                                                293 SerGluProGlyProAlaPhePro------ThrGlnProGlnLysThrGln 307
                                                                                                                                                                                                                                                                                                                                                               Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF238383 938 bp mRNA linear EST 05-AUG-20
AGENCOURT 15097797 NICHD XGC Emb6 Silurana tropicalis cDNA clone
IMAGE:6993385 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Genomics
National Cancer Genomics
National Cancer Institute / MIH
Bldg. 31 Rm10A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencoutt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
                                                                                                                                                    249 CysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGly
                                                                          758 TGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGTGATCAGCTGGGGTGAGGGCTGTGCC
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1 (Bases I to 938)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                               878 GATCATCCCCAAACTGCAGTTCCAGCCAGCGAGGTTGGG----CGGCCAGAAGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------CACCATCCTGCTGCTCCTCCCAGCGCTGCTGTT 1018
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Matches:
Conservative:
Mismatches:
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High quality sequence stop: 724.
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/db_xref="taxon:8364"
                                                                                                                         269 ArgArgAsnArgProGlyValPhe---
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Location/Qualifiers
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINIA at: http://image.llnl.gov Series: IRAK Plate: 52 Row: d Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13994275 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCAACACCTCTGAGACGTCCTG---TACCAGGTCTGCTGGGGGGCAAGGCAGCTAGTG 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCCTGACGGCTGCGCACTGCTTC---- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 AsnGlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAsp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsn--- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 creraccascecacceccrccascecicascersescersescersescenses 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyThrAlaCysTrpAlaThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               638 TÁCAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACÁTGCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AlaArgGlyProProTyrCysGlyArgProGluProSerAlaArgIleValGlyGlySer 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysGlyGlySerLeuIleAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1188
128
32
118
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                         note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                             1. ,1188
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-037-417-46 (1-357) x BC034294 (1-1188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555.50
50.79%
40.63%
28.44%
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578
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----MetThrAsnGlyThrLeuGluProAlaAlaGluTrpSer 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 LeuArgieuAlaSerProAlaSerLeuGlyProAlaValTrpProValCysLeuProArg 162
                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
                                                  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
E 1 (bases 1 to 777)
S Govoroum, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
L Unpublished (2003)
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23-48.50.09
Fax: 02.23-48.50.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="tcba0009c.j.09"
/tismuc_type="multi-tissues"
/dev stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="Rainbow trout multi-tissues (tcba)"
/clone_lib="Weator: pT713D-pac, Clone distribution : AGENAE
Resource centre. François PIUMI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 cecrecaaececearririgiedadecrererrareaacaagagiedededece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisGlyGlyHisIleCysGlyGlySerLeuIleAlaProSerTrpValLeuSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Radiobiologie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Francois Piumi@jouy inra fr, INRA, CEA Radiobiologie
Brude du genome (IARG), Domaine de Vilvert, 78352,
Jouy-en-Josephere, FRANCE, +33 (0) 1.34.65.28.02,
(0) 1.34.65.22.73"
                                                                                                                                                                                                                                                                                                                        chromatogram of
                                                                                                                                                                                                                                                                                Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions.
at sigenasupport@jouy.inra.fr to obtain the chromatogra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777
108
35
95
16
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Oncorhynchus mykiss"
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Matches:
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-037-417-46 (1-357) x BX860661 (1-777)
                                                                                                                                                                                                                                                                                                                                                                Plate: 0009 row: j column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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56.30%
42.52%
28.16%
                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: M13R.
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Query Match:
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  SOURCE
                                                                                                              AUTHORS
TITLE
                                                                                                                                                                        JOURNAL
                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EX860661 Rainbow trout multi-tissues (tcba) Oncorhynchus mykiss CDNA clone tcba0009c.j.09 Sprim, mRNA sequence.
EX860661
EX860661.1 GI:39958625
                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                    342
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                                                                                                                                                                                                                                                                                                                                                                                                                                             402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 GluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArg 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 ArgAsnArgPro-GlyValPheThrAlaValAlaThrTyrGluAlaTrpIleArgGluGl 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808 GCCAACGCACCGGGGGGTCTATAACCAAAGTCCAGTATTATGACTCTTGGATCAAACGTA 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 nValMetGlySerGluProGlyProAlaPheProThrGlnProGlnLysThrGlnSerAs 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ccittcattaaaarcagcgaaagcaggarcagcactgg 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGlu 195
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                                                                                                                                  77
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                                                                                                                                                                                                                                                  78 AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPro 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  748 AATGTCAACAACACGTGGTGGCAGTATGGCATCATCAGCTGGGGTATTGGATGTGCTGAA
                                                                                                                                                                                                  TGGCCCTGGCAGATCAGCCTGAGCTAAAGGTCAAACTGTCTGCGGAGGAAGCCTTATC
                                                                                                                                                                                                                                                                                                                                                                  GTTTCTCAATACATTGTTTACCTTGGAGTTTAT---CAACTGTCTAACCTTAAAAACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 GGATACAAGGAAGGACAGATAGATGCCTGTCAGGGAGACTCTGGTGGGCCCTCTTGTATGC
                                                                                              CysGlyArgProGluProSerAlaArgIleValGlyGlySerAsnAlaGlnProGlyThr
                                                                                                                                                                          TrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySerLeuIle
                                                                                                                                                                                                                                                                                                                              AlaalaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                             343 AATACGGTATCTAGTGGGGGTGAAAAGAATCATCATAAACAAGGCTTACCAATACGAGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGluLeuArgleuLeuGlyGluAlaThrCysGlnCysLeuTyrSer---
                                                                                                                                                                                                                                                                            ACCGACAGCTGGGTTCTGACTGCTGCTCACTGCTTTGATTCG
    25
    Indels:
Gaps:
                                                          (1-938)
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                                                          (1-357) x CF238383
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    28.21%
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on Dec 10, 2002 this sequence version replaced gi:12836502.

please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptuse prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. Second strand CDNA was prepared with the primer adapter of sequence[5] strand cDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence[5] strand CDNA was prepared with the primer adapter of sequence transcripted to the primer adapter of sequence transcripted to the primer adapter of sequence transcripted to the primer adapter of the primer adapter of the primer adapter of the primer adapter of the primer adapter of 
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                 Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                 6. (Dages 1 to 3025),

8. Adachi, J., Atahira, S., Akimura, T., Arai, A., Aono, H.,

8. Adachi, J., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

8. Arakawa, T., Bono, H., Tara, A., Hayateu, N., Hiramoto, K.,

8. Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,

8. Kaukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

8. Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

8. Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,

8. Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,

8. Saito, H., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y.,

8. Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,

7. Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,

7. Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

Direct Submission Door, Norbiki, A., Maranishi, The Institute of
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/db_xref="MGI:1904397"
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/strain="C57BL/6J"
                                                                                                                                                                   of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3035)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                           362 GAGGACAGCACCTACGCTGGCACTAATAGCTGGGTCACCGGATGGGGCGATATCAAT 421
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mus musculus (house mouse)
Mus musculus
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Oy 293 SerdluProdlyProAlaPheProThrdlnProdlnLysThrGlnSerAspCys 310 2505 TACAGAGCTGCC	AY419856 Homo sapiens ST14 gene, VIRTUAL TRANSCRIPT, genomic survey sequence. AY419956 AY419956 AY419956 AY419956 AY419956 AY419956.1 GI:39775813 GSS. Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vermanalia; Eutheria; Primates; Catarrhini; Flammalia; Eutheria; Primates; Catarrhini; Flammalia; Eutheria; Primates; Catarrhini; Flammania; Eutheria; Primates; Catarrhini; Flammania; Derrica, S., Wang, G., Zheng, X.H., White, T., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-ord, M.A., Tanenbaum, D.M., Civello, D.R., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Todd, M.D. and Cargill, M. Direct Submission	Pred. No.: 8.05e-32 Leulous: 13.5 Score: 540.09 Matches: 13.3 Percent Similarity: 54.09\$ Conservative: 39 Percent Similarity: 40.21\$ Mismatches: 34 Query Match: 27.65\$ Gaps: 7 US-10-037-417-46 (1-357) x AY419856 (1-2487) Qy
DCGLGGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIADRWVITAAHCFOEDSM ASFKLWTVFLGXRRQNSRNFGEVSFKVSRLFLHPYHEEDSHDYDVALLGLDHPVVYSA TVRPVTLBYRGNSRNFFEPCQHCWITGWGAQREGGPVSNTLGKDHVVYSA TVRPVINTIQVIT" POlyA_signal	38 C	

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/tissue type="embryo, stage 17/19"
/lab_host="DH10B (phage-resistant)"
/clone lib="NICHD XGC Emb2"
/note="Vector: pCWV-SPORT6; Site_1: Not1; Site_2: Sal1;
cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 MetThrAsnGlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHisSer 109
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                                                        Contact: Robert Strausberg, Ph.D.
Email: ggapbs-rémail.nih.gov
Tissue Profurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10808 row: 1 column: 22
High quality sequence stop: 691.
    National Cancer Institute, Cancer Genome Anatomy Project (CGAP) Tumor Gene Index Gene Index Unpublished (1997)
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:8355"
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1660 AGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAG 1719
                                                                                                                                                                  1780 GCGGATGAGGGCGAGTGGCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATC 1839
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1 (bases 1 to 905)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                        --SerAlaArglleValGlyGlySerAsn
                                                                        1720 GACTGCGACTGTGGGGTCGTTTCACGAGACAGGCTCGTGTTGTTGGGGGGCACGGAT
                                                                                                                                                                                                                                                                                                   92 AsnGly-----ThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHisSer
                                                                                                                                                                                                                                                                                                                                                                                      Gln---AspGlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AlaGlyTyrProGluGlyArgArgAspThrCysGlnGlyAspSerGlyGlyProLeu---
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                                                                                                                         AlaGlnProGlyThrTrpProTrpGlnValSerLeuHisHis---GlyGlyGlyHisIle
                                                                                                                                                                                                               CysGlyGlySerLeulleAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThr
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              208 CysLeuTyrSer------GlnProGly---ProPheAsnLeuThrLeuGln 221
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Search completed: February 25, 2004, 18:01:10 Job time: 2501 secs

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Scoring table:

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APPLICANT: Darrow, Andrew
APPLICANT: Andrede-Gordon, Patricia
APPLICANT: Andrede-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine;
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION VUMBER: US/09/387,375
CURRENT APPLICATION VUMBER: US/09/387,375
WUMBER OF SEQ ID NOS: 9
US-09-907-794A-262

US-09-905-125A-262

US-09-902-775A-262

US-09-902-775A-256

US-09-905-71A-15

US-09-905-71A-256

US-09-905-775A-256

US-09-023-942A-5

US-09-023-942A-25

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US-09-016-366A-24

US-09-116-10

US-09-106-36A-24

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Patent No. 6485957
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SEQ ID NO 1
LENGTH: 1613
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Best Local Similarity:
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Pred. No.:
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Sequence 8,
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1: /cgn2_6/ptOdata/2/ina/5A_COMB.seq:*
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                 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-386-642-8
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US-09-3875-8
US-09-386-642-7
US-09-644-600-1
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Listing first 45 summaries
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Sequence 8, Application US/09386642 Patent No. 6420157 GENERAL INFORMATION: APPLICANT: Darrow, Andrew

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Conservative:
Mismatches:
APPLICANT: Qi, Jenson
APPLICANT: Addraded-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICANTION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1142
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150 SerLeuGlyProAlaValTrpProValCysLeuProArgAlaSerHisArgPheValHis 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACAGCAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGGCTGTGC
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                                438 CCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACG
                                                                                                        498 decargaacriecriedercacriedecriededagececeagreadeagacerecrecreedeaa
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE TEREBROE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 LeuHisGlnThrAlaPheLeuAspSerAlaArgIle 322
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Sequence 431, Application US/09620312D
Patent No. 6569662
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_FL_genes Version 1.0
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Tanag, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
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Yang, Yonghong
Wang, Jian-Rui
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an, Tom
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                                       261
                                                                                                             hrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThrAlaValAlaT 281
                                                                                                                                  TGAGCTGGGGAATGCCTGTGGGGCCCGCAACAGGCCTGGTGTACACTCTGGCCTCCA 832
                                                                                                                                                                                    301
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                                     lyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleT
                                                                                                                                                                                    hrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluProGlyProAlaPheProT
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                                                                           GTGACTCTGGGGGCCCCACTCTCCTGCCCTGTGGAGGGTCTCTGGTACCTGACGGGCATTG
                                                                                                                                                                                                                                                        -----CysLeuHisGlnThrAlaPhe 316
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09386653A;
Fatent No. 645864
GENERAL INFORMATION:
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Datable Gordon, Patricia
APPLICANT: Datable Gordon, Patricia
TITLE OF INVENTION: DA encoding the novel human serine;
TITLE OF INVENTION: DA encoding the novel human serine;
TITLE OF INVENTION: DATABLE TO STATE OF THE REFERENCE: ORT-1032;
CURRENT APPLICATION NUMBER: US/09/386,653A.;
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 1110
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Conservative:
Mismatches:
Indels:
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28.85%
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Best Local Similarity:
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Query Match:
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                                        ThrGlnProGlnLysThrGlnSerAspCys
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                                                                     1016 edecchegagececerrengageagererecheckeechgeecegeera
                                                                                                                                                                                                      Sequence 30 Application US/09023942A
Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John TITLE OF INVENTION:
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: POSIOL/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
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Conservative:
Mismatches:
Indels:
                                                                                                         311 LeuHisGlnThrAlaPheLeuAspSerAlaArgIle 322
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                                                                                                                                                                                                                                                                                                                               ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 111.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEFAX: (516) 742 4366
TELEFAX: 650 901 SANS UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         STATE: NEW YORK
                                                                                                                                                                               RESULT 5
US-09-023-942A-30
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Mismatches:
Indels:
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Matches:
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51.28%
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US-09-620-312D-431
                                                                   sapiens
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Best Local Similarity:
Query Match:
            EQ ID NO 431
LENGTH: 1212
TYPE: DNA
ORGANISM: HOMO S
                                                                                                  NAME/KEY: CDS
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Pred. No.:
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OTHER INFORMATION: Description OTHER INFORMATION: sequence of
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1130
                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                      6.91e-37
557.00
56.63%
45.78%
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Best Local Similarity:
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Pred. No.:
                                                                                                                      US-09-387-375-8
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Sequence 8, Application US/09387375
Sequence 8, Application US/09387375
Patent No. 648595'
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Q1, Jenson
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION NUMBER: US/09/387,375
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of Artificial Sequence: Nucleic acid
EOS zymogen fusion gene
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Matches:
Conservative:
Mismatches:
Indels:
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us-10-037-417-46.p2n.rni

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ProleuValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPhe
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-027-337-1
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Matches:
Conservative:
Mismatches:
Indels:
                                                                        Sequence 7. Application US/09386642;
Sequence 7. Application US/09386642;
Sequence 7. Application US/09386642;
GRNERAL INFORMATION:
APPLICANT: Darrow andrew APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Parricia
APPLICANT: Andrade-Gordon, Parricia
APPLICANT: Andrade-Gordon, Parricia
TITLE OF INVENTION: Zymogen Activation System
FILE OF INVENTION: Zymogen Activation System
FILE OF INVENTION: 27028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT PILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO
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2063 CAGAGCCAGGCGCCCTGGGGTGCAGGAGCGCAGGCGCATCATCTCCCAC 2122
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Sequence 1, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed i
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REPERBENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
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GlycysclyArgArgAsnArgProClyValPheThrAlaValAlaThrTyrGluAlaTrp
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2393 GTGGGCTTCCTCAGCGGCGCGTGGACTCCTGCCAGGGGGGATTTCCGGGGGGACCCCTGTCC 2452
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2063 CAGAGCCAGCGCAGCGCCCTGGGGTCCAGGAGCGCAGCATCATCTCCCAC 2122
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                                                                 1763 AGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAG 1822
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                                                                                                           --SerAlaArglleValGlyGlySerAsn
                                    32 AlaArgGlyProProTyrCysGlyArgProGluPro-
US-10-037-417-46 (1-357) x US-09-644-600-1 (1-3147)
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Sequence 18, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
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|TG-----ATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACCACCTGCGAGAAC 2356
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         129 AlaAsnTyrSerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerPro 148
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; Sequence 1, Application US/09644600
; Patent No. 6451500
; General Information:
Applicant: O'Brien, Timothy J.
Applicant: O'Brien, Timothy J.
TILE OF INVENTION: TAGG-15. An Extracellular Serine Protease
TILE REPERENCE: D664C1P/D;
CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR PILING DATE: 1999-02-20
; PRIOR PILING DATE: 1998-02-20
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ORGANISM: Homo sapiens
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                                            248 ValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCys
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APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REPERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/654,600A
CURRENT FILING DATE: 2000-09-01
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09/027,337
PRIOR FILING DATE: 1999-10-20
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TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFRENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
FRIOR APPLICATION NUMBER: 09/421,213
FRIOR APPLICATION NUMBER: 09/421,213
FRIOR APPLICATION NUMBER: 09/027,337
FRIOR APPLICATION NUMBER: 09/027,337
FRIOR APPLICATION NUMBER: 09/027,337
FRIOR FILING DATE: 1998-10-20
FRIOR FILING DATE: 1998-02-0
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US-09-644-600-18
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ORGANISM: Artificial sequence
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Percent Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                               HisGlyThrAlaCysTrpAlaThrGlyTrpGlyAspValGlnGluAlaAspProLeuPro 188
                                                                                                                                                                                                                                                                  149 AlaSerLeuGlyProAlaValTrpProValCysLeuProArgAlaSerHisArgPheVal 168
                                         Gln---AspGlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValPro 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 ValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuProTrpValLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCys
                                                                                                                                                                                                                                                                                                     209 LeuTyrSerGlnProGlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 Aladiy1rvrproGluGiyArgArgAspThrCysGlnGlyAspSerGlyGlyProLeu---
                                                                                                                                                          129 AlaAsnTyrSerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerPro
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Sequence 18, Application US/09654600A

Patent No. 6649741

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CALIMOTO, Hirotoshi
TITLE DF INVENTION: TANG-15: An Extracellular Serine Protease
TITLE DF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CHERENT FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 09/421,213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3147
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PRIOR FILING DATE: 1999-10-20
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NUMBER OF SEQ ID NOS:
SEQ ID NO 18
LENGTH: 3147
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Pred. No.:
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FILE REPERENCE: 10466-14

CURRENT FILING DATE: 2010-02-22

PRIOR APPLICATION NUMBER: US 60/144, 048

PRIOR PLILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146, 222

PRIOR APPLICATION NUMBER: US 60/146, 222

PRIOR APPLICATION NUMBER: US 60/146, 222

PRIOR PLILING DATE: 1999-07-26

PRIOR PLILING DATE: 1999-07-26

PRIOR PLILING DATE: 1999-09-08

PRIOR PLILING DATE: 1999-09-13

PRIOR PLILING DATE: 1999-09-13

PRIOR PLILING DATE: 1999-09-13

PRIOR PLILING DATE: 1999-09-13

PRIOR PLILING DATE: 1999-11-30

PRIOR PLILING DATE: 1999-11-30

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PRIOR PLILING DATE: 1999-11-30

PRIOR PLILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PLILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PLILING DATE: 1999-12-02

PRIOR PRILING DATE: 1999-12-02

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PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PLILING DATE: 1999-12-02

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PRIOR APPLICATION NUMBER: PCT/US99/3099

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PRIOR PLILING
                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Sequence 262, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                        Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E.
                                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Baton, Dan L.
                                                                                                                                                                                                              Fong, Sherman
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ORGANISM: Homo Sapien
US-09-907-794A-262
                                                                                                                                                                                                                                                                                                       Goddard, A.
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Mismatches:
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               PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PELING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PCT/US99/28565
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APPLICATION NUMBER:
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US-09-905-125A-262
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LENGTH: 1378
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AVERYATION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-0.22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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PRIOR PLING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-09-15
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  955 TGGGGCCCTCAGGGCACCGAGCCAGGGCT-CTGGGGCCGCCGCGCGCTCCTAGGGCGCAG 1013
                                                                                                                               328 SerHislleSerVal---------GlyValSerThrGlyThrLysSerLeu 341
                                          308 SerAspCysLeuHisGlnThrAlaPheLeuAspSerAlaArgIleLeuLeuArgProLeu 327
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Patent No. 6664376
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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APPLICANT: Genentech, Inc.,
APPLICANT: BAFLEGAN; AVI
APPLICANT: BOLSTEIN, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Mather, Jennie P.
Pan, James
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SerglyglyProleuvalCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSer 262
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PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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Patent No. 6686451
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Goddard, A.
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                                                ProLeuProLeuProTrpValLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThr 205
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494 GAGCGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATC 553
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-De-/Capt. 1/USPTO spool p/US10037417/runat 24022004_101040_17563/app_query.fasta_1.519
-De-Published Applications Na -OFMT=fastap -SUFETX=p3n.rmbb -MINMATCH=0.1
-DB-Published Applications Na -OFMT=fastap -SUFATEL -END=1 -MATRIX-b10sum62
-LOOPCIL=0 -LOOPEXT=0 -UNITED-16 -START=1 -END=1 -MATRIX-b10sum62
-TRANS-buman40.cdi -LIST=45 -DOOALIGN=200 -THR SCORE-pct -THR MAX=100
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-NORD=6 -ICPU=3 -NO MMAP -LARGEQUERY -NOS GCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV TIMBOUT=120 - WARN_TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-LONGLOG -DEV TIMBOUT=120 - YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                          (without alignments)
3133.050 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
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                                                                                                                        2004, 17:20:05 ; Search time 399 Seconds
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                            Conservative:
Mismatches:
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; Sequence 85, Application US/10176847; Publication No. US20030068636A1; GENERAL INFORMATION: ; APPLICANT: Veiby, Petter Ole

US-10-176-847-85

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BREAST
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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF TITLE OF INVENTION: AND OVARIAN CANCER FILE REFERENCE: MRI-039
CURRENT APPLICATION NUMBER: US/10/176,847
CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 85
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    216 PheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArg
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APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
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         AAGANGCCTGCCAGGGTGACTCTGGGGGCCCACTCTCCTGCCTGTGGAGGGTCTCTGG
                                                                        GlnThrAlapheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer
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APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Mcthods of Detecting Cancer Based on Prostasin
FILE REFERENCE: 81994/282423
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT PILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
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Patent No. US20020090625A1
GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L41351
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FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2214
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ORGANISM: Homo sapiens
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                       236 ArgaspincysgindlyaspserglyglyprojegualcysglugluglyglyArgirp
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John MONAHAN
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 36 ProTyrCysGlyArgProGluProSerAlaArgileValGlyGlySerAsnAlaGlnPro
                                                        56 GlyThrTrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySer
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Sequence 261, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:

US-10-097-340-261

RESULT 6

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Molecules and Proteins For The Identification, Prevention, and Therapy of Ovarian Cancer
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Matches:
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CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT PILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR PILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-6

PRIOR FILING DATE: 2001-03-6

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

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PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules TITLE OF INVENTION: Assessment, Prevention
                                                                                                                                                                                                  Peter VEIBY
Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                Sebarian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                         Rosemarie SCHMANDT
Xumei ZHAO
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LENGTH: 1834
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TYPE: DNA

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CACCTGGCCTTCAGCTCTGCCCCAAGCCCTTGCTGAGGCCCATCCTTTTCCTGCCT 1212
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GluproAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAsp 115
                            116 GlyalaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGlu 135
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ctcgaggtgcctctgatcagtcgtgagacgtgtaaactgcctgtacaacatcgacgccaag
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                                                                                     559 GACGCCAAGGTCAGCACCCTGAAGGACATCCTCCCCCACCCCAGCTACCTCCAAGGAGGGC
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GENERAL INFOGRATION:
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERRACE: 1517.0012
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PREFERRACE: 2.001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 48 PATENTIN VER. 2.1
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US-10-101-510-447
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160
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133
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                                  Length:
Matches:
Conservative:
                                                                                                       US-10-037-417-46 (1-357) x US-10-101-510-447 (1-3382)
                                                                                                                                                                    21 TyrserleuTyr---GlyLeuValProSerGlyPro--
                                                               Mismatches:
Indels:
                                    1.76e-53
697.00
55.29%
42.33%
35.69%
sapiens
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
 Homo
    ;
US-10-101-510-447
                             Alignment Scores:
Pred. No.:
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
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Patent No. US20020052308A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and TITLE OF INVENTION: Nucleic Acids, Proteins and TITLE OF INVENTION: NUCLEIC ACIDS, Proteins and FILE REPRENCE: PAIO6
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NOS: 1694
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Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Bdinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
                                                      Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
Smithson, Glennda
Gunther, Erik
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Miller, Charles E
Guo, Xiaojia
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PRIOR APPLICATION NUMBER: US 60/280,509
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/311,055
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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1076 GICTICAGCTCAGCGCAGCCCCGAAATIGTTAAGGCCCGTACTTTTCCTGCCACTTGGT 1135
                                                                                                                                                                               298 AlaPheProThrGlnProGlnLysThrGlnSerAsp-----CysLeuHisGlnThr 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        성
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Proteins, Polymucleotides Encoding Them and Methods TITLE OF INVENTION: Using the Same FILE REFERENCE: 21402-537
258 AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr
                                                                                                                    962 CTGACTICTACCTAIGCTICCTGGAICCACCACCATGTG-----GCAGAGCTCCAGCCT
                                                                                                                                                                                                                                                                       315 AlapheLeuAspSerAlaArg---IleLeuLeuArgProLeuSerHisIleSerValGly
                          278 AlavalAlaThrTyrGluAlaTrplleArgGluGlnValMetGlySerGluProGlyPro
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CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 00/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                     334 ValSerThrGlyThrLysSerLeu 341
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Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Bllerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Padigaru, Muralidhara
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Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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Miller, Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smithson, Glennda
Gunther, Erik
Stone, David
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138 AlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpPro 157
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                                                                                                                                                               274 GlyvalPheThrAlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySer 293
CysGlyArgProGluProSerAlaArg1leValGlyGlySerAsnAlaGlnProGlyThr
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                                                                                                254 ArgrrpheGlnAlaglyrleThrSerPheGlyPheGlyCysGlyArgArgAsnArgPro
                               dlyargargarpTnrcysGlnGlyaspserGlyGlyProteuValcysGluGluGlyGly
                                                       1613
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; Sequence 1, Application US/10041400A
; Bublication No. US20020110895A1
; GENERAL INFORMATION:
; APPLICANT: Barrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
; TITLE OF INVENTION: Protease EOS
; FILE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/09/14,400A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1613
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Mismatches:
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Best Local Similarity:
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|CAGCAACTCGAGGTGCCTCTGATCGTGAGACGTGTAACTGCCTGTACAACATCGAC 831
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                                                                                                                                                                                                                                                               MetAlaGlnLysGlyValLeuGlyFroGlyGlnLeuGlyAlaValAla
                                                                                                              1161
134
45
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                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                               Length:
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                                                                                                               2.7e-46
612.00
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CRGANISM: Homo sapiens
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                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HisArgPheValHisGlyThrAlaCysTrpAlaThrGly 177
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                                                                                                                                                                                                                                                                                                                                                                  CTGGGGGGCGCTGCGGCTCCACCTCGCCCCGCACG 380
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Length:
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972 CAGGCACCTGCCTATACCCCACATCCCTTCTGCCTCGAGGCCAAGATGCCTAAAAAAG-- 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 GlyvalpheThralavalAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySer 293
                                                                                                                                                                                                                                                                                                254 ArgirpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAshArgPro
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Publication No. US20040005557A1
GENERAL INFORMATION:
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
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Shenoy, Stacie J
Gaman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
Pena, Carol EA
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Herrman, John L
Peyman, John A
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Zerhusen, Bryan D
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Miller, Charles E
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APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT FILING DATE: 2002-01-08
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                            APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William M
APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: DENCTEINS, POLTNUCLEOTIDES
TITLE OF INVENTION: DENCTEINS, POLTNUCLEOTIDES
TITLE OF INVENTION: DENCTEINS, POLTNUCLEOTIDES
TITLE OF INVENTION: DENCTEINS, POLTNUCLEOTIDES
TITLE OF INVENTION: DENCTEINS, POLTNUCLEOTIDES
TITLE OF INVENTION: UNMER: 60/26,595
PRIOR PELING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-01-18
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PRIOR FILING DATE: 2001-01-18
                    Kekuda, Ramesh
Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
Liu, Kiachong
Bllerman, Karen
Rothenberg, Mark
Stone, David J
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AX436567 Sequence
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AX1351 Homo sapien
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-MODEL=frame+p3n.model-DEV=xlp
-MODEL=frame+p3n.model-DEV=xlp
-De_cgnz_1/USPTO spool_p/US1003/417/runat_24022004_101108_18083/app_query.fasta_1.519
-De_cgnz_1/USPTO spool_p/US1003/417/runat_z40.2002.000001
-DESCADENTAL -OFWT=fastap_SUPFIX=olip2n.rge -MINMATCH=0.1_-LOOPCL=0 -LOOPEXT=0
-DOCALIGN=200 -THR_SCOEE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL_OUTFMT=pto
-NORM=ext -HEAPSIXE=500 -MINIEN=0 -MAX.ENB=20000000
-USER=US10037417_@CGN_1_1_4958_@runat_1_ALIGN=10108_18083 -NOCU=6 -ICPU=3
-NO.MAP -LARAGOURRY -NEG_SCORES=0 -WAIT -DSPBICCK=100 -LONGLOG
-DGT_THROUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDEFXT=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                   - nucleic search, using frame_plus_p2n model
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Kekuda, R., Alsobrook, J.P., Tchernev, V.T., Liu, X., Spytek, K.A., Patturajan, M., Grosse, W.M., Lepley, D.M., Burgess, C.E., Vernet, C.A., Li, L., Gorman, L., Edinger, S., Sciore, P., Ellerman, K., Malyankar, U., Rothenbergy, M., Strone, D., Boldog, F., Shenoy, S. and Anderson, D. Proteins and nucleic acids encoding same batent: WO 02053742-A 45 11-JUL-2002; Curagen Corporation (US)
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Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A.,
Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U.,
Rothenberg,M., Stone,D., Boldog,F., Shenoy,S. and Anderson,D.
Proteins and nucleic acids encoding same
Patent: WO 02053742-A 43 11-UUL-2002;
Curagen Corporation (US)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
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                                                                                             Plowman,G., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. Charydczak,G.
Novel proteases
Patent: WO 2000860-A 52 03-JAN-2002;
Sugen, Inc. (US)
                                                         Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Butelo
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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272
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Conservative:
Mismatches:
Indels:
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             GI:18675722
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76.19%
                                   Homo sapiens (human)
Homo sapiens
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AX360096.1
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Best Local Similarity:
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                                      TACTCACTTTACGGGTTGGTGCCGTCCGGACCCGCTAGGGGCCCCCCGTACTGCGGGCGC
                                                                                                                   GlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySerLeuIleAlaProSer
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AX360096
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217

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PAT 13-FEB-2002

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Primer for synthesizing full-length cDNA and use thereof.
BD127529
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JP 2002017375-A/2960
22-JAM-2002
07-JTL-2000
JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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PC
CI2N15/09, CO7K14/47, CO7K16/18, CI2N1/15, CI2N1/19, CI2N1/21, CI2N5/ PC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 2010)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                      531
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Primer for synthesizing full-length cDNA and use thereof FH K
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GCCGACCTGGCCCTGCTGCCCTCGCCTCGCCAGCCTGGGCCCCGCCGTGTGGCCT
                                  ValCysLeubroArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
                                                       YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2960
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SIPI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, SHINICHI KOJIMA,
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/db_xref="taxon:9606"
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JP 2002017375-A/2960.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0246383-A 31 13-JUN-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 2681
                                                           772 GCAGGAATCACCAGCTTTGGCTTTGGCTGTGGACGGGAAACCGCCCTGGAGTTTTCACT
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Sequence 31 from Patent WO0246383.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AK075142. GI:22761040
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Homo saplens (human)
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TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Ota,T.; Nishikawa,T.; Isogai,T.; Hayashi,K.; Ishii,S.; Kawai,Y.; Ota,T.; Nishikawa,T.; Nagai,K.; Kojima,S.; Otsuki,T. and
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                                                                                                                                                                                                LeuIleAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeu
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                                                                                                                                                          Koga,H.

Frimer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 200201375-A 650 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 200201375-A/650
PP 22-JAN-2002
PP 07-JUL-2000 JP 200223172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SPI ISHII,
PI SHII,
PI YURI KAWAI,AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGA.
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                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                        SerGlnAspGlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValPro
                                                                                                                            Xiao, Y. and Morozov, V. Regulation of human prostasin-like serine protease Patent: WO 0198467-A 1 27-DEC-2001; Bayer Aktiengesellschaft (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Sequence 1 from Patent W00198467.
AX342934
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Homo sapiens (human)
JP 2002017375-A/1916
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Key
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   OS Homo sapiens (human)
DE 22-JAM-2002
PD 22-JAM-2000
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUJ PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUJ PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUJ PI TOSHIO OTA, TETSUJI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
PI TETSUJI OTSUKI, HISASHI KOGA
PC
CIZNIS/09, CO7K14/47, CO7K16/18, C12NI/15, C12NI/19, C12NI/21, C12NI5/
                                                                                                                                                                                                      C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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Sequence 3 from Patent WO0198467.
AX342936
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1 (bases 1 to 670)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.
                                                             C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                                                                              C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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Primer for synthesizing full-length cDNA and use thereof.
BD126485.1 GI:23221430
JP 2002017375-A/1916.
Homo sapiens (human)
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                                                                                                                                                              /organism='Homo sapiens (human)'
Location/Qualifiers
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                           TETSUJI OTSUKI, HISASHI KOGA
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              SHINICHI KOJIMA
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1. (bases 1 to 127769)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
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                                                                                                                                                                                                                                                                                                                                       121 AlavalAlaAlaIleValValProAlaAsnTyrSerGlnValGluLeuGlyAlaAspLeu
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                                      serine protease
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Matches:
Conservative:
Mismatches:
                    Xiao,Y. and Morozov,V.
Regulation of human prostasin-like ser
Regulation of human prostasin-like ser
Patent: WO 0198467-A 3 27-DEC-2001;
Bayer Akriengesellschaft (DE)
Location/Qualifiers
1. 456
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Direct Submission
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Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
Submitted (103-APR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94599, USA 10 127769)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission

Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Brive, Walnut Creek, CA 94598, USA

5 (bases 1 to 127769)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission

Particular Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 233.4kb). It is clipped at the overlap with AC135050. The number of bases overlapped is 2575.
                                                                                                                                                                                                                                                                                                                                                                                                               www.jgi.doe.gov
Prin:shing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
                                                                                                                                                                                                                                                                                                  Submitted (29-MAR-2003) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA On Mar 29, 2003 this sequence version replaced gi:29029216. Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 GlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31349 GCCTGCTGGGCCACCGGCTGGGAGACGTCCAGGGGGA 31311
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
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                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                   /mol_type="genomic_DN
/db_xref="taxon:9606"
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Consensus quality: 18238 bases at least Q30
Consensus quality: 188035 bases at least Q30
Consensus quality: 188035 bases at least Q30
Consensus quality: 188035 bases at least Q30
Consensus quality: 188035 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agn-of-contigs estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                         Direct Submission
Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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9058: gap of unknown length
11051: contig of 1993 bp in length
11151: gap of unknown length
13741: contig of 2490 bp in length
13741: gap of unknown length
17738: contig of 3997 bp in length
1738: contig of 1997 bp in length
1738: contig of 4192 bp in length
1738: contig of 4192 bp in length
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g of 9267 bp in length
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gap of unknown length
contig of 1166 bp in length
gap of unknown length
contig of 1509 bp in length
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of 4872 bp in length
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of 5717 bp in length
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contig of 1136 bp in length
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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                                                                                                                                                                                                                                                                                                          Center Project Name: 809609
                                                                                                           Unpublished
2 (bases 1 to 195476)
DOE Joint Genome Institute.
                                                              1 (bases 1 to 195476)
DOE Joint Genome Institute.
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7722:
7822:
Homo sapiens (human)
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                  Homo sapiens
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                  ORGANISM
                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                              REFERENCE
AUTHORS
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AC106629 232119 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-21802, WORKING DRAFT SEQUENCE, 2
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 SerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 GlyproLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 GlyProAlaValTrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThr
873 101972: gap of unknown length

1973 117076: contig of 15104 bp in length

1077 117176: gap of unknown length

1974 138973: contig of 21797 bp in length

1974 139073: gap of unknown length

1074 150336: contig of 11283 bp in length

1337 150436: gap of unknown length

1004150: contig of 11280 bp in length

1004150: gap of unknown length

100416: contig of 45040 bp in length.
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/clone="CTD-2551B20"
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
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Draper H. Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls T., Fan, G., Francer, C.M., Gabisi, A., Garta, R., Garcia, A., Garner, T., Gabisi, A., Garta, R., Garcia, M., Garrer, T., Gabregororgis, E., Geer, K., Gill, R., Garcia, M., Garra, M., Gunarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Hernandez, J., Hollins, B., Howells, S., Hildwish, J., Idolenird, D., Jackson, A., Hollins, B., Howells, S., Hildwish, J., Idolenird, D., Jackson, K., Garchall, J., Garcol, L., Jang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, K., Johnson, K., Johnson, E., Johnson, K., Johnson, K., Johnson, K., Marchin, E., Liu, W., Loulseed, H., Lozado, R.J., Lavis, L., Marchin, E., Mandhartne, M., Marnoud, M., Malloy, K., Mangum, B., Manhindartne, M., Martin, K., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mandhartne, M., Mangum, B., Mandhartne, M., Mangum, B., Mangum, B., Mandhartne, M., Mangum, M., Morris, S., Munidasa, M., Morris, S., Morris, S., Munidasa, M., Morris, S., Mandhartne, M., Mangum, B., Mandhartne, M., Mangum, M., Martin, S., Mandhartne, M., Mangum, B., Mandhartne, M., Mangum, M., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mandhartne, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, R., Martin, R., Reilly, M., Ren, Y., Reuer, M., Reigh, M., Ren, Y., Reves, R., Reger, R., Riggs, F., Reilly, M., Ren, Y., Reves, R., Reger, R., Righ, R., Saderer, S., Soott, G., Shatsam, S., Shen, H., Sheetty, J., Sharts, M., Shatsam, S., Tingey, A., Trejos, Z., Umani, K., Walle, F., Wallson, M., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R., Walle, R
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Loudite acquencing Consolition.

Submitted (13-MAY-2003) Human Gencene Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23604383.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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.----- Project Information
Center project name: GL93
enter clone name: CH230-21802
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Direct Submission
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AUTHORS
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AUTHORS
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JOURNAL
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COMMENT

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AC117170

244161 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-20P9, *** SEQUENCING IN PROGRESS ***,
5 unordered pieces.
                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Assembly program: Atlas 3.0;
Consensus quality: 222629 bases at least Q40
Consensus quality: 223625 bases at least Q30
Consensus quality: 224449 bases at least Q20
Estimated insert size: 234994; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 ProGlyThrTrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 SerLeuIleAlaProSerTrpValLeuSerAlaAlaHisCysPhe 89
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Rattus norvegicus (Norway rat)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .232119
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
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site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BZ109922"
128621. .230127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end_sequence:BZ109921"
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100.00%
9.80%
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Best Local Similarit
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table.

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Anyalebechi, V., Aoyagi, A., Ayodeji, W., Baca, E., Badh H.,
Baldhin, D., Bildharama Bia, Rebung, K., Mitth, P., Barced, M., Banhmed, F.,
Bryant, N., Bhay, C., Hutch, P., Birteli, K., Calderon, E.,
Bryant, M., Bhay, C., Hutch, P., Birteli, K., Calderon, E.,
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COMMENT

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data.html).
                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.)

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25619: contig of 25619 bp in length 25719: gap of unknown length 137872: contig of 112153 bp in length 137972: gap of unknown length 240790: contig of 102818 bp in length 241970: contig of 1080 bp in length 242070: gap of unknown length 242070: gap of unknown length 242070: gap of unknown length 244161: contig of 2091 bp in length.
                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine Center code: BCM
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                            129868 CCTGGCRCTTGGCCGTGGCAGGTGAGCCTGCATCACGGTGGAGGCCACATCTGCGGGGGC 129927
                                                                                                                                                                                          AC093520 168064 bp DNA linear PRI 19-MAR-2003
Homo sapiens chromosome 16 clone RP11-120K18, complete sequence.
AC093520
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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hinshing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Exrors is 0.
Location/Qualifiers
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOB Joint Genome Institute.
Direct Submission
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Submitted (31-MG-2001) Production Sequencing Facility, DOE Joint
Submitted (31-MG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 168064)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168064)

10 Dob Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
Uppublished
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74
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                                                                                                     129928 FCCCTCATGGCCCCTTCCTGGGTCCTCCGCTGCTGTTTC 129972
                                                                                    SerLeulleAlaProSerTrpValLeuSerAlaAlaHisCysPhe
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DOE Joint Genome Institute.
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Search completed: February 25, 2004, 23:28:10 Job time : 3995 secs

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Human pro DNA encod

Nucleotid

Human cDN Human pro

OM protein

Run on:

Sequence:

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Human; NOVX; neurological disorder; Alzheimer's disease;

Huntington's disease; Parkinson's disease; pain; behavioural disorder;

Huntington's disease; Parkinson's disease; pain; behavioural disorder;

Mutoimmune disease; myasthenia grands; asthma; arthritis; diabetes;

Mutoimmune disease; myasthenia grands; asthma; arthritis; diabetes;

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Mutoingtis, forensic biology; transgenic animal; drug screening;

Mutoingtis forensic biology; transgenic animal; drug screening;

Mutoingtis description; mortility in the chromosome 16; gene; ds.
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 Command line parameters:

-MODEL=frame+_D2n.model -DBV=x1p
-MODEL=frame+_D2n.model -DBV=x1p
-Q=/Cqn12 1/USPF0 spool p/USI/0037417/runat__24022004__101108__18072/app__query.fasta_1.519
-Q=/Cqn2 1/USPF0 spool p/USI/0037417/runat__spool = MINMATCH=0.1 -LOOPCL=0
-LDOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-USTRAT=1 -SCORE=quality -TRR MIN=1 -ALIGNE=15 -MODE=LOCAL
-UISTRAT=pto -UNITS=bits -STRAT=1 -END=-1 -MATRIX=0ligo -TRANS=human40.cdi
-USTRAT=pto -UNITS=bits -STRAT=1 -END=-1 -MATRIX=200000000
-USER=USI/0037417_@CGN 1 1 885 @runat__24022004 101108 18072 -NCPU=6 -ICPU=3
-NO WARP -LARGEQUERY -NEG SCORES=0 -MALT -DSPBLCK=100 -LONGLOG
-DSP TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=60 -YGAPEXT=6 -DELOP=6 -DELEXT=7
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(without alignments)
3619.586 Million cell updates/sec
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Aak94500 B
Abk13565 B
Aa869040 B
                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                      - nucleic search, using frame_plus_p2n model
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cDNA enco Gene #221

Kidney ca Kidney ca

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Human bre Human ova Other;

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353 G; 216

BP; 162 A; 371 C;

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The invention relates to 24 novel human proteins designated NOV1-NOV14

(ABB09501-ABB09524), collectively referred to as NOVX proteins, and
nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and
nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and
concleted disorders or in the manufacture of a medicament for treating
such disorders are associated with NOVX proteins including neurological
disorders are associated with NOVX proteins including neurological
disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
confercal cancer, leukaemia and osteosacoma), immune disorders
conforced and cancer, leukaemia and osteosacoma), immune disorders
conforced and cutcimmune disorders, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular diseases
conforced and autoimmune disorders, and parkinson's disease,
conforced and autoimmune disorders, and particularly cardiomyopathy,
alberteins of arthritis, scleroderma, alopedia, ulcers, pancreatitis,
continence, psoriasis, scleroderma, alopedia, ulcers, pancreatitis,
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disorders, obesity, bacterial infections and particularly cardiomyopathy,
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disorders, obesity, bacterial infections or downstream effectors which
continence, psoriasis, wound healing and angiogenesis. NoVX
contention, haematopoiesis, wound healing and angiogenesis. NovX
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contentifying and cloning NOVX homologues in other cell types Cells
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'product= "NOV14a"
/note= "No stop codon given in the specification"
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; 2001US-026036P.
; 2001US-027241P.
; 2001US-0272817P.
; 2001US-0303231P.
; 2001US-031840SP.
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10-SEP-2001;
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                                                               1038
                                    321 ArgileleuleuArgProleuSerHisileSerValGlyValSerThrGlyThrLysSer 340
                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation; proliferation; motility; haematopolesis; wound healing; angiogenesis; forensic biology; transgenic animal; drug screening; gene therapy; NOV14b; prostatin precursor-like; gene; ds.
                                                                                                                                                                                                                                                                                Huntington's disease; Parkinson's disease; pain; behavioural disorder; addiction; tuberous sclerosis; cancer; immune disorder; allergy; autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
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Grosse WM, Lepley DM, Burgess CE, Vernet CAM,
nger S, Sciore P, Ellerman K, Malyankar U;
Stone D, Boldog F, Guo X, Shenoy S, Anderson D
aupier RJ, Miller CE, Eisen A;
                                                                                                         1039 CTTGTCCTCCCCTGGCTCTCTCCACACTCTCTCTGGGCCTCTGGGGGTTC 1089
                                                                                        LeuValLeuProTrpLeuSerProHisSerLeuLeuGlyLeuTrpGlyPhe 357
                                                                                                                                                                                                                                                                      Human; NOVX; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                            Human prostatin precursor-like NOV14b DNA, SEQ ID NO:45.
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19. 1092
/*tag= b
/product="NOV14b"
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02-MAR-2001; 2001US-0272817P.
05-JUL-2001; 2001US-03303231P.
12-JUL-2001; 2001US-0318405P.
10-SEP-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318700P.
04-JAN-2002; 2002US-00037417.
                                                                                                                                                                    ABQ93902 standard; DNA; 1102 BP.
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Gorman L, Edinger S, Sc.
Rothenberg M, Stone D, 1
Padigaru M, Taupier RJ,
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08-JAN-2001;
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The invention relates to 24 novel human proteins designated NOV1-NOV14

(ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleotides are useful in the treatment, diagnosis or prevention of NOVX-nucleotides are useful in the manufacture of a medicament for treating associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24 NOVX proteins, based on their homology to known proteins. Various disorders (e.g., Albrahmer's B. Huntington's and Parkinson's disease), disorders (e.g., Albrahmer's B. Huntington's and Parkinson's disease), pain, behavioural disorders, addiction, tuberous sclerosis, cancers pain, behavioural disorders, disperation, tuberous sclerosis, cancers of incorrectal cancer, leukaemia and osteosarcoma, immune diseases), mischerosis, actual disorders, disperation, immune diseases, arious forms of arthritis diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, actual continence, psoriasis, scleroders, logorders, endometriosis, cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine cirrhosis, glomerular receptors or denomeration of mall molecules that modulate or inhibit processes such be used to identify cellular receptors or downstream effectors which are nucleic acids and solves for the binds to a NOVX protein, and are also useful as argets for the binds to a NOVX protein, and are also useful and producing non-human configuration, haematopolesis, wound healing and any openesis. Or proliferation, haematopolesis, wound healing and ending NOVX mucleic acids are useful as a source of primers or probes for corensic biology and for care useful as a source of primers or probes for producing mon-human cores, and any pro
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Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune
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                                                                                                                                                                                                                          Claim 9a; Page 143; 323pp; English.
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Best Local Similarity:
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Caenepeel

Manning G,

Sudarsanam S,

Whyte D,

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The present invention relates to the isolation of novel human proteases, and the mucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and disorders (e.g. restenosis and disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. restenosis and carmatoria arthritis and pooriasis), central or peripheral nervous system of diseases, migratines, pain, sexual dysfunction, mood disorders, attention disorders, hypotension, hypertension, psychotic disorders, neurological disorders, hypotension, hypertension, psychotic disease, and polypeptides are also cuseful for treating viral infections caused by human immunodeficiency over the HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (e.g. virus (HIV)).
                                                                                                                                                                                                                                            Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences encoding for the novel human proteases of the invention
                                                                                                                                                                                                                                                                                                                                      Claim 26; Fig 18S-TT; 313pp; English
                                              26-JUN-2001; 2001WO-US020171
                                                                             26-JUN-2000; 2000US-0214047P
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                                                                                                                 (SUGE-) SUGEN INC
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Sequence 2457 BP; 377 A; 851 C; 797 G; 432 T; 0 U; 0 Other;
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Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection;

ocular disease; cytostatic; gene; ds.

WO200200860-A2 Homo sapiens

encoding novel human protease #52.

DNA

(first entry)

23-APR-2002

ABK31795

BP.

ABK31795 standard; DNA; 2457

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05-DEC-2001; 2001WO-US046964.

13-JJN-2002

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The invention relates to an isolated Protein Modification and Maintenance diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMM. These include gastrointestinal disorders (e.g. Crohm's disease), cardiovascular disorders (e.g. Crohm's disease), cardiovascular disorders (e.g. proliferative disorders), developmental disorders (e.g. anaemia), cell proliferative disorders, developmental disorders (e.g. scabies), neurological disorders (e.g. Alzheimer's disease) reproductive disorders (e.g. ectopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the effects of exogences compound on the expression of nucleic acid and amino acid sequences of protein modification and maintenance molecules. The invention, encoding a polypeptide which has been found to have homology
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Au-Young J, Elliott VS;
, Lu DAM, Lee EA;
MG, Khan FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.
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Hafalia AJA, Ga
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08-DEC-2000; 2000US-0254399P.
21-DEC-2000; 2000US-0257603P.
05-UAN-2001; 2001US-0260110P.
19-UAN-2001; 2001US-02681EP.
25-UAN-2001; 2001US-0264623P.
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Walia NK,
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and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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GCCGACCTGGCCCTGCTGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCCGTGTGGCCT
                               ValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
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Kojima S, Otsuki T, Koga
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K, Koji
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Wakamatsu A, Sugiyama T, Nagai
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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; vividide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atterosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease (e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, infection. The human prostasin-like serine protease gene provides a therappeutic target of decreasing human prostasin-like serine protease atthe protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention comprises the cDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease purified from human seminal fluid. An antibody specific for prostasin-like serine protease is useful for immunodetection and diagnosis of micro-metastases, autoimmune lesions and renal failure in blopsy specimens, plasma samples and body fluids. The antibody may be
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20-MAR-2001; 2001US-0276909P.
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augment and inhibit the enzyme activity which may be useful to treat osteoprosis; Paget's disease and degradation of bone implants is particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proliferation and liphibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to
                                                                                                                 diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #1 nucleotide sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                 536 CTCATCGCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGCTG
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Homo sapiens

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    LeuProTrpValLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCys
                                                                                             LeuTyrSerGlnProGlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCys
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                                                                                                                                                                                           AlaGlyTyrProGluGlyArgArgAspThrCysGln 240
                                                                                                                                                                                                                  GCTGGCTACCCAGAGGCCGCAGGGACACCTGCCAG 447
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02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                              AAK92190 standard; cDNA; 670
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Wakamatsu A, Sugiyama T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypetide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 597 BP; 97 A; 217 C; 196 G; 87 T; 0 U; 0 Other;
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG04853.
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Best Local Similarity:
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                       830 Primers useful for synthesizing full length cDNA clones and their use
   Kawai Y;
T, Koga I
                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 650; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 670 BP; 97 A; 245 C; 205 G; 118 T; 0 U; 5 Other;
Isogai T, Hayashi K, Ishii S,
a T, Nagai K, Kojima S, Otsuki
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representative sequence

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                                                                                     PheMetThrAsnGlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHis
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            1177 GGGGGCTCAAACGCGCAGCCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGT
                                                                                                                                                                                                                        AlaSerLeuGlyProAlaValTrpProValCysLeuProArgAlaSerHisArgPheVal
GlyGlySerAsnAlaGlnProGlyThrTrpProTrpGlnValSerLeuHisHisGlyGly
                                           GlyHisIleCysGlyGlySerLeuIleAlaProSerTrpValLeuSerAlaAlaHisCys
                                                        Ishii S, Kawai Y;
S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone representative sequence, SEQ ID NO: 1916.
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K, Kojima
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su A, Sugiyama T, Nagai
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02-MAY-2000; 2000JP-00183765
                                                                                                                                                                                                                                                                                                                                       AAK93456 standard; cDNA; 670
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special

330 Primers useful for synthesizing full length cDNA clones and their use

genetic manipulation.

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WPI; 2001-524255/58.

Example 11; SEQ ID NO 1916; 1380pp + Sequence Listing; English.

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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; autiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genetmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation;
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methods. The present sequence was used as the representative sequence
from a human clone which was used in homology searches to identify the
clone. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AlaAsnTyrSerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerPro
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                                                                                                                                                                                                                                                                     Length:
Matches:
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Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                             Disclosure; Fig 3; 111pp; English
      23-JUN-2000; 2000US-0213588P.
20-MAR-2001; 2001US-0276909P.
                                                     WPI; 2002-114576/15
                                       Morozov V;
                         (FARB ) BAYER AG
                                       Kiao Y,
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This invention comprises the cDNA and protein sequences of an isolated protestasin-like serine protease and reagents and methods for requlating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease is useful for immunodetection and for prostasin-like serine protease is useful for immunodetection and inpay specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atheroscierosis, neurodegenerative disease (e.g. prion protein amyloid plaques of Genstmann-Straussles Syndrome, creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease gene provides a chimic, in particular for treated the control of decreasing human protestism protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #2 nucleotide sequence of the invention

Sequence 456 BP; 74 A; 151 C; 167 G; 62 T; 0 U; 2 Other;

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                                                                                                                                                                               12.1 AlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGluLeuGlyAlaAspLeu
                                                                                                                                                                                                             384 GCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGAGCTGGGCGGCGACCTG
                                                                                                                                                                                                                                                                                                                                            161 ProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGlyTrpGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                            181 ValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGluLeuArgLeu
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Conservative:
                                                           Mismatches:
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  Length:
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Sequence 2298 BP; 468 A; 774 C; 706 G; 350 T; 0 U; 0 Other;

Alignment Scores:

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coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                   221 GlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAspThrCysGln
                             144 CTGGGCGAGGCCACCTGTCAATGTCTTACAGCCAGCCCGGTCCCTTCAACCTCACTCTC
                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                           DNA encoding novel human diagnostic protein #6883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 6883; 103pp; English.
                                                        241 GlyAspSerGlyGlyProLeuVal 248
                                                                   24 GGTGACTCTGGGGGGCCCCTGGTC
                                                                                                                   AAS71079 standard; cDNA; 2298
                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
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483
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                                                                                                                                                                                                  AlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluProGlyPro 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted polypeptide; nervous disease; muscular disease; tummour; agstrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; renal gland disease; small intestine disease; colon disease; lippase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection.
                                                                                                                                        AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr
                                                                                                                                                        GCAGGAATCACCAGCTTTTGGCTTTTGGCTGTGGAAACCGCCCTGGAGTTTTCACT
                                                                                                                                                                                                                               GCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCTGGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a human secreted polypeptide.
                                                                                                                                                                                                                                                               AlaPheProThrGlnProGlnLysThrGlnSerAsp 309
                                                                                                                                                                                                                                                                                         GCCTTTCCCACCCAGAGACCCAGTCAGAT 579
 Length:
Matches:
Conservative:
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                                                Mismatches:
                                                             Indels:
                                                                             Gaps:
                                                                                                           (1-2298)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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13-MAR-2000; 2000US-0188916P.
03-OCT-2000; 2000US-0236874P.
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9.73e-38
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*tag=
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                                                Similarity:
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                                Percent Similarity:
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   Pred. No.:
                                                Best Local
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The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, consmall intestine, heart, trachea, thymnus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation such as myocardial infarction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating liver diseases, coagulation disorders and microbial diseases, for treating limens and microbial diseases, for treating immune disorders, for treating inflammation and transplant rejection, for enhancing bone thickness and increasing apoptosis, and for regulating vascular ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGTGGCCACATCTGCGGGGGGCTCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinfilammatory; anti-HIV; antibacterial; vulnerary; attiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nervous system related polynucleotide SEQ ID NO 13567.
                                                                                                                                                                                                                                                                                                              Sequence 768 BP; 125 A; 280 C; 224 G; 139 T; 0 U; 0 Other;
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Conservative:
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24-FEB-2000;
02-MAR-2000;
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17-MAR-2000;
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PR 79-WX-2000 2000US-020551EP.
PR 70-UIN-2000 2000US-021513EP.
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PR 21-SEP-2000 2000US-023141P.
PR 21-
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RR 20-CGT-2000; 2000ES-2047086P.

RR 20-CGT-2000; 2000ES-204708EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

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RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

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RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

RR 20-CGT-2000; 2000ES-204718EP.

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RR 20-CGT-2000; 2000ES-204718EP.

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RR 20-CGT-2000; 2000ES-204718EP.

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RR 20-CGT-2000; 2000ES-204718FP.

RR 20-CGT-2000; 2000ES-204718FP.

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RR 20-CGT-2000; 2000ES-204718FP.

RR 20-CGT-2000; 2000ES-204718FP.

RR 20-CGT-2000; 2000ES-204718FP.

RR 20-
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ΜÄ,

Patturajan M, Vernet CAM, Guo X, Boldog FL, Grosse , Rothenberg ME, Ellerman I, Peyman J, Smithson G;

Gangolli EA, Burgess CE, Pat Tchernev VT, Miller CE, Gud JP, Garlach V, Edinger S, I V Stone DJ, Millet I,

Macdougall J,

Gunther E,

Zhong M, C Taylor S, Alsobrook

2002-590674/63.

P-PSDB; ABB98416

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isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing in (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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The present sequence is a coding sequence for a NOV protein. The NOV associated disorders or in the manufacture of a medicament for treating the disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthmatigh nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases, NOVI4b is a prostasin-like protein, and the NOVI4b coding sequence localises to

chromosome 16

NOVX polypeptides and encoding polynucleotides, useful for preventing or treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or

Claim 9; Page 99; 358pp; English.

pharmacogenomics.

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Human; NOV14a; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Ancectic; Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; Antibacterial; Neuroprotective; Nootropic; Antibacterial; Virucide; Antiparastitic; Relaxant; Anticonvulsant; Gene Therapy; NOV; cancer; heart disease; inflammation; autoimnum disorder; Albergy; blood disorder; AlbS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis, arthritis; Alzheimer's disease; inflection; stroke; muscular dystrophy; epilepsy; wasting disorder; prostasin-like protein; chromosome 16p11.2; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaGlnLysGlyValLeuGlyProGlyGlnLeuGlyAlaValAla 16
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/product= "NOV14a"
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Best Local Similarity:
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Location/Qualifiers

/product= "NOV14b"

WO200255704-A2

18-JUL-2002

1. .1161 /*tag= 8

Spytek KA;

Shenoy S,

Casman SJ,

Li L, Zerhusen BD,

Padigaru M,

(CURA-) CURAGEN CORP.

18-APR-2001; 28-FEB-2001; 09-MAR-2001;

2001US-0260417P. 2001US-0260831P. 2001US-0272338P.

09-JAN-2001; 10-JAN-2001;

2001US-0274876P 2001US-0284704P

09-JAN-2002; 2002WO-US000554.

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NOVX polypeptides and encoding polynucleotides, useful for preventing treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                            Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM; Taylor S, Tchernev VT, Miller CE, Guo X, Boldogo FL, Grosse WM, Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K, Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G; Gunther E, Stone DJ;
                                  09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-0272338P.
09-MAR-2001; 2001US-0284704P.
          09-JAN-2002; 2002WO-US000554.
                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                      WPI; 2002-590674/63.
P-PSDB; ABB98415.
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or

The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, unch as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, IgA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitio), strok, muscular dystrophy, epilepsy, and other wasting disorders associated with chornic diseases. NoV14a is a prostasin-like protein, and the NoV14a coding sequence localises to chromosome 16p11.2 Sequence 1726 BP; 284 A; 581 C; 499 G; 362 T; 0 U; 0 Other; Claim 9; Page 97-98; 358pp; English.

1726 16 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 9e-05 16.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Score:

US-10-037-417-46 (1-357) x ABN85392 (1-1726)

Search completed: February 25, 2004, 22:21:32 Job time: 431 secs

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CB996389 AGENCOURT
BF063417 7489e10.x
BF063417 7489e10.x
BF063810.y
A1658798 LU08909.x
BG482000 602527844
A1393068 L925e09.x
BM837284 K-EST0113
BR280845 601155410
BM837589 K-EST0113
BR37565 K-EST0113
BR37569 K-EST0113
BR37565 K-EST0113
BR37565 K-EST0026
BG479276 602526495
CB125988 K-EST0174
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BG386531 602455771
BQ292219 PM2-AN008
AU134797 AU134797
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AZ252377 RPCT-23-4
BB850607 BB850607
AZ875648 2M0190113
BB850564 BB850564
BU164841 AGENCOURT
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BM828821 K-EST0101
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A1623099 tu49f05.x
A1193435 qe58e10.x
CB116948 K-EST0161
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BF561257 UI-R-C0-h
AA996811 UI-R-C0-h
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537)
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1414920-1417921,1520940-1522439); NCI CGAP GC4 pool 1 LLAM
1267096-1258631,1469064-1470983, 1475592-1476743);
NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE CIONEIDS 986759,1101192-1101959,
1217928-1220615); NCI CGAP Colo pool 1 LLAM 2644-2653,
2871-2872 (IMAGE CIONEIDS
1057416-1061255,1145984-1145351). (10% of the driver population), plus a pool 0 3,840 arrayed clones from NCI CGAP Subl (IMAGE CIONEIDS 2708616-2710535) and NCI CGAP Subl (IMAGE CIONEIDS 2708616-2710535) and NCI CGAP Subl (IMAGE CIONEIDS 2708616-2710535)
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                                                                                                                                                                                                                                                                                                   Email: cgapbs remail.nib.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
POLYA-NO.
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            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
AUTHORS
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100 GluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAlaHisThr
                 Conservative:
Mismatches:
              Length:
Matches:
                                                           Indels:
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           8.71e-127
154.00
100.00%
100.00%
43.14%
                                              Similarity:
                                 Percent Similarity:
Best Local Similari
Alignment Scores:
Pred. No.:
                                                        Query Match:
                        Score:
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120 ArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGluLeuGlyAlaAsp

GAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGCCCCCTGGACGGCGCGCACACA

à g

FEATURES

COMMENT

456 bp mRNA linear EST 28-OCT-1998 qd49f07.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1732837 3' similar to SW:MCP6_MOUSE P21845 MAST CELL PROTEASE 6 PRECURSOR ;, mRNA sequence. cededagrescescarceresrescesceacracracasecaacrasses estas 199 165 219 105 220 LeuGlnileLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgArgThrCys 239 primer [5' double-stranded cDNA was size selected, ligated to Eco KI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco KI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung 104 ciccadaiairidecadagardergrergecraecraecadagececeagagacacede Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), 344 chédecenderedecendeceneacedechadechadecedecedecendialenene 160 LeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGlyTrpGly 284 CTGCCCCCCCCTCACACCCCTTCGTGCACGCCACCCCCTGCTGGGCCACCGCTGGGGA 180 AspvalGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGluLeuArg 224 GACGICCAGGAGGCAGAICCICIGCCICICCCCGGGGGGCTACAGGAAGTGGAGCTAAAGG Contact: Contact Strausberg, Ph.D.
Contact: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 712 Std Error: 0.00 LeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpProValCys 200 LeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyProPheAsnLeuThr 240 GinglyAspSerGlyGlyProLeuValCysGluGluGlyGly 253 CAGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAAGGCGGC 3 /organism="Homo sapiens" Insert Length: 712 Std Brror: Seg primer: -40UP from Gibco High quality sequence stop: 452. Location/Qualifiers /clone="IMAGE:1732837" /mol_type="mRNA" /db_xref="taxon:9606" /sex="unknown" AI190509.1 GI:3741718 Homo sapiens (human) (bases 1 to 456) Tumor Gene Index Unpublished (1997) 1. .456 Homo sapiens 404 140 44 source RESULT 2 AI190509/c DEFINITION ORGANISM AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE REFERENCE JOURNAL

Pred. No.:

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Alignment

DRIGIN

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/clone="CSOCAPOINGI"
/tissue type="THYMUS"
/clone=Tib="Homo sapiens THYMUS"
/note="Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMvSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF561257
296 bp mRNA linear EST 12-DEC-2000
UI-R-CO-hh-h-07-0-UI.rl UI-R-CO Rattus norvegicus cDNA clone
UI-R-CO-hh-h-07-0-UI.5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                  University of lowa 155 MEBRF, Iowa City, IA 5242, USA 71-1319 335 9256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
This clone will be available through Research Genetics (www.resgen.com)
LINL (info@image.llnl.gov). IMAGE ID= 1781449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metaus
Eukaryota; Meterias; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherias; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                        253 GlyargrrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCySGlyArgArgAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 ProGlyValPheThrAlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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Mismatches:
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|strain="Spraque-bawley"
|db_xref="taxon:10116"
|clone="Ul-R-CO-hh-h-07-0-Ul"
|dev_stage="adult"
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3-PRIME, mRNA sequence.
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1 (base 1 to 930)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAPO01AD09FM1&cluster=7995.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO01AD09FM1.
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                                                                                                                                                                                                                                                      141 AlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTroProValCysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BMail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7995.f
more liformation about this cluster, see
                                                                           456
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                                                                         Length:
Matches:
Conservative;
Mismatches:
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NbHL19W."
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                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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                                                  Scores:
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221

24

RESULT 3
BX436299
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE JOURNAL COMMENT

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FEATURES

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Similarity:
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/lab_host="DH10B (Life Technologies)"
/clone_lib="UT-R-CO"
/clone_lib="UT-R-CO"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia)
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-AI
library consisted of unraped normalized libraries
constructed from tat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-EI
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
normalized libraries constructed from 8, 12 and 18-day
normalized libraries constructed from 9, 12 and 18-day
normalized libraries constructed from 9, 12 and 18-day
normalized libraries constructed from 9, 12 and 18-day
normalized libraries constructed from 61-sent
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from
pool of UI-R-AI and UI-R-EI clones from which 3' ESTS had
been derived was used as a driver in a hybridization with
the pooled UI-R-AI and UI-R-EI library in the form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA996811
UT-R-CO-hh-h-07-0-UI.S1 UI-R-CO Rattus norvegicus CDNA clone
UI-R-CO-hh-h-07-0-UI.3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [ (bases 1 to 322) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   use pourted of a contract of the standard single-stranded single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to hydroxyapatite column chromatography, converted to bacteria (life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB Coordinated Laboratory for Computational Genomics
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Rattus norvegicus
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TITLE
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/lab_host="vector: pr773D-Pac (Pharmacia) with a modified
/note="vector: pr773D-Pac (Pharmacia) with a modified
/note="vector: pr773D-Pac (Pharmacia) with a UI-R-CU
polylinker; Site 1: Not 1; Site_2: Eco RI; The UI-R-AI
library is a subtracted library derived from the UI-R-AI
wixture of individually tagged normalized libraries
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, voary, and muscle. The UI-R-EI
kidney, heart, spleen, voary, and muscle. The UI-R-EI
library consisted of a mixture of individually tagged
normalized libraries constructed from $1.2 and 18-day
normalized libraries constructed from $1.2 and 18-day
endryor. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dr track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified CDNA inserts from a
pool of UI-R-AI and UI-R-EI library in the form of
the pooled UI-R-AI and UI-R-EI library in the form of
circles (subtracted library) was purified by
circles (subtracted library) was purified by
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Email: bento-soares@ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
oligo-dr track not found, Not I site shown in Preparation: M.
is likely internal to the message. cDNA Library Preparation: M.
statina Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LINL (info@image.llnl.gov). INAGE
ID=1781449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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/clone="UI-R-C0-hh-h-h-07-0-UI"
                                                                                                                                                                                                                                                                                                                                                                       'organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="Sprague-Dawley"
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BY236668
BY236668.1 GI:26417846
EST.
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ORGANISM

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE 1 (bases 1 to 365)

R (Azaki,Y.; Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N.; Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagai,K., Tomaru,Y., Hasegawa,Y., Mogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Harelor,S., Palsiel,R., M., Blake,J.B., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,B., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T., Gasipori, T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T., Gasipori, Gasipori, T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T., Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipori, Gasipor
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                                                                                                                                                                                                                      /tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
Indels:

    .351
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="C57BL/6J"

                                                                                                                                                        /db xref="taxon:10090"
/clone="F930049D04"
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                                                                                                                Mammaliar Eucherla; Rodentia; Sciurconathi; Muridae; Murinae; Mus. Mammalia; Eucherla; Rodentia; Sciurconathi; Muridae; Murinae; Mus. Nikaido.]., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, J., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schrim, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, Y., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, B., Lyons, P.B., Kanashani, T.A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.B., Magnehima, T., Marchonni, L., Makens, P., Mathi, H., Nagashima, T., Read, J.C., Reck, D.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, K., Pontius, J.U., Qil, D., Kamachandran, S., Ravasi, T., Reed, J.C., Red, D.J., Reid, J., Ring, B. Z., Ringwald, M., Sultana, R., Takenka, Y., Taylor, M.S., Taesdale, K.D., Tomita, M., Verardo, R., Wanner, L., Wanner, L., Wanner, C., Semple, C.A., Setou, M., Shimada, K., Sangiawa, M., Yang, I., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Wang, T., Kawai, J., Aizawa, K., Sato, K., Shinagawa, R., Tasuki, R., Sakai, W., Sato, K., Shinaki, T., Wang, T., Kawai, J., Aizawa, K., Itoh, M., Kagawa, T., Pukuda, S., Hara, A., Hashizume, M., Emoteni, R., Shinagawa, R., Yasunishi, A., Soshino, M., Waterston, R., Landerien, R., Shinagawa, R., Yasunishi, A., Soshino, M., Waterston, R., Landerien, M., Rogens, J., Bitiney, E., and Hayashizaki, Y., Waterston, R., Landerien, M., Radawa, T., Pukuda, S., Hara, A., Hashizume, M., Sasaki, D., Bitiney, M., Radawa, T., Pukuda, S., Hara, A., Hashizume, M., Waterston, R., Landerien, M., Radawa, M., Waterston, M., Waterston, R., Landerien, M., Radawa, M., Waterston, M., Waterston, R., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
For Intuity of Bhysical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus (house mouse)
Mus musculus
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22354683 12466851

JOURNAL MEDLINE PUBMED COMMENT

TITLE

FEATURES

JOURNAL MEDLINE

PUBMED

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Mus musculus
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Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
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Human Genome Sequence Mamm. Ganome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapilary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
nonredundant conta lime sequence clustering for construction of a
cDNA library was prepared and sequence clustering for construction of a
cDNA library was prepared and sequence in Musse Genome
Encyclopedia Project of Genome Exploration Research Group
Bivision of Experimental Animal Research in Riken
Division of Experimental Animal Research in Riken
                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Schenes Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 55 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gos.riken.go.jp) for further details.
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BY236911 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930050D15 5', mRNA sequence.
BY236911
BY236911.1 GI:26418099
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     Contact: Yoshihide Hayashizaki
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EcoR1; Site_2: ECOR1; Female C57BL/6J mouse kidney and/or
brain genomic DRA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DRA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Moublished (1999)
Other_GSSS: RPCI-23-466N15.TJ RPCI-23-466N15.TVB
Contact: Shaying Zhao
Contact: Shaying Zhao
Contact: Shaying Zhao
Contact: Shaying Chao
Contact: Shaying Chao
Contact: Shaying Chao
Contact: Shaying Chao
Contact: No. Rockyille, MD 20850, USA
The Institute for Genomic Research
Fex: 301 838 0208
Fex: 301 838 0208
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Akinrel,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhaogtigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.biffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.rigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 466 row: N column: 15
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ocation/Qualifiers
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Dupublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9216
Email: genome-resegsc.riken.go.jp,
URL:http://genome-sesc.riken.go.jp,
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

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1 (Dases) 1 to 433)
1 (Asimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Konino,H., Konda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sagaki,Y., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Tanaka,T., Tomaru,A., Togawa,A., Takahashi,F., Takaku-Akahira,S.,
Muramatsu,M. and Hayashizaki,Y.
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Shibata, K., Itoh, M., Carninci, P., Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ875648 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0190113F Genomic survey sequence.
                                                                                                                                                                                                                                                                          /clone="F930108E12"
|tissue type="inner ear"
|dev_stage="adult"
|clone lib="RIKEN full-length enriched, adult inner ear"
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Insert Length: 10000 Std Brror: 0.00
Plate: 0190 row: I column: 13
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Sag primer: CGTTRAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 454.
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/organism="Mus musculus"
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                                                                                                                                                                                                                           /mol_type="mRNA"
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/db_xref="taxon:10090"
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Fax: 801 585 7177
                                                                                                                                                            e mouse tissues.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinaes. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMPAQ (gif 4732114/gbl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (Dases I to 433)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayateu,N., Hiramcoc,K., Hiraoka,T., Furuno,M., Hanagaki,T.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Ishii,Y., Ito,M., Sawai,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Solio,R., Sakio,R., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sagabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
RIKEN Bncyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
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BB850564
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/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clome lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42zv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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'organism="Mus musculus"
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Smail: cgapbs-r@mail.nih.gov
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                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--184-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. (10), 1757-171 (2000)

Sugahara,Y. and Hayashizaki,Y. Shibata,K., Itoh,M., Carninci,P., Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                  Email: genome-resignscriken.go.jp,

VRL:http://genome.gsc.riken.go.jp/
Carninci.p./.Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

and Hayashizaki,Z., Muramatsu,M., Inoue,Y., Kira,A.

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/clone_lib="RIKEN full-length enriched, adult inner ear"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                       Contact: Yoshihide Hayashizaki
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1..875
| organism="Homo sapiens"
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| mol_type="mRNM" |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 22-MAY-2003
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I (bases 1 to 907)
NIH-WGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Bmail: cgapbs-romail.nih.gov
Tisgue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: NDAM447 row: j column: 12
Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLnage.llnl.gov. d column: 24 High quality sequence stop: 645.
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IMAGE:30383555 5', mRNA sequence.
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Location/Qualifiers
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Homo sapiens
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/...*../
/ organism="Homo sapiens"
// mol_type="mRNA"
// mol_type="mRNA"
// db_xref="taxon:9606"
// clone="IMAGE:6651279"
// clone="IMAGE:6651279"
// lab hofe="mHJUB (phage-resistant)"
// lab hofe="mHJUB (phage-resistant)"
// lone lib="NHJ MGC 107"
// note="Organ: breast; Vector: pOTB7; Site_1: EcoR1;
// note="Organ: breast; Vector: pOTB7; Site_1: EcoR1;
// note="Organ: DNA made by oligo-dT priming
// inctionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University ing Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
// Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
       /clone="IMAGE:3083555"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone lib="NIH MGC 180"
/note="Cogan: Testis, Vector: pcWv-SPORT6.1; Site 1: Not1;
Site 2: EccRv (destroyed); Library is oligo-dT primed and directionally cloned (EccRv site is destroyed upon cloning). Average insert size 1.68 kb; Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM2897 row: n column: 15
High quality sequence stop: 423.
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AGENCOURT 10435504 NIH_MGC_107 Homo mapiens cDNA clone INAGE: 6651279 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mil.nih.gov
Tissue Procurement: ATCC
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db_xref="taxon:9606"
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Alignment Scores:

ORIGIN

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Pred. No.: 0.000182 Length: 929
Score: 17.00 Matches: 17
Best Local Similarity: 100.00$ Conservative: 0
Duest Match: 13
Best Local Similarity: 100.00$ Mismatches: 0
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Search completed: February 26, 2004, 00:06:29 Job time: 2502 secs

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Patent No.

1, Appli 10, Appli 1, Appli 5, Appli 6, Appli 6, Appli 7, Appli 7, Appli 7, Appli

Sequence Sequence (

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Seguence Sequence

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Sequence

Patent No. 522 Sequence 22,

Sequence 44, Sequence 46, Sequence 58,

Sequence

Sequence Sequence

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Sequence Sequence

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US-09-280-116-72/c

Sequence 72, Application US/09280116A

Sequence 72, Application US/09280116A

Patent No. 6331427

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INFORMATION:

FILE REFERENCE: 5800-24, 035800/176965

CURRENT APPLICATION NUMBER: US/09/280,116A

CURRENT FILING DATE: 1999-03-26

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NOS: 268

SOFTWARE: PatentIN Ver. 2.0
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Conservative:
Mismatches:
Indels:
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US-09-280-116-72
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  TYPE: DNA
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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2042.448 Million cell updates/sec
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1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
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                                                               February 25, 2004, 18:59:12; Search time 97 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: / Ggn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                             nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-280-116-72
US-09-244-111-3
US-09-00-526-1
US-09-008-271A-19
US-09-386-642-9
US-09-618-259-72
US-09-618-259-6
US-09-280-116-28
US-09-280-116-29
US-09-280-116-29
US-09-80-116-29
US-08-906-616-122
US-08-906-616-122
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  682709 seqs, 277475446 residues
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                                                                                                                                                                60.0
60.0
7.0
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60.0 , Ygapext 6
6.0 , Fgapext
6.0 , Delext
                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
                                                                                                            US-10-037-417-46
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Match Length
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792
9442
10449
13443
262
3460
486
436
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Ygapop
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Perfect score:
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                                               protein
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Maximum DB
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                                                                   Run on:
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Result

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Pred. No.:
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TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
FILE REFERENCE: PR391
CURRENT APPLICATION NUMBER: US/09/244,111
CURRENT FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 60/073,961
EARLIER APPLICATION NUMBER: 60/073,961
SARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 792
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329 TGCCAGGGTGATTCCGGAGGCCCGCTGGTGTGTGAGGAA 291
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ZIP: 19482
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
971.1NG DATE: 30.APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6100059
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCUTTAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
ITILE OF INVENTION: No. 6100059el Compounds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                       Sequence 3, Application US/09244111
Patent No. 6566498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
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REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.00
100.00%
100.00%
3.64%
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (85)..(708)
US-09-244-111-3
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Best Local Similarity:
Query Match:
                                                                                                                 GENERAL INFORMATION:
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US-09-070-526-1
                                                        US-09-244-111-3
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237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys 249
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APPLICANT: Bandman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
CCMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-037-417-46 (1-357) x US-09-070-526-1 (1-944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
REFERENCE/DOCKGT NUMBER: G
TELECOMMUNICATION INFORMATION
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                    13.00
100.00%
100.00%
3.64%
                                                    TELERA: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                  0.00149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                  linear
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Best Local Similarity:
                                                                                                                                                                                                ; TOPOLOGY: li
; MOLECULE TYPE:
US-09-070-526-1
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DB:
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TYPE: DNA ORGANISM: artificial sequence
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                           Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-618-259-72/c
; Sequence 72, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease; FILE REFERENCE: D6020C192
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; NUMBER OF SEQ ID NOS: 72
; LENGTH: 1343
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Matches:
Conservative:
Mismatches:
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                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                                                                               US-10-037-417-46 (1-357) x US-09-008-271A-19 (1-994)
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFRENCE: ORT-1028
CURRENT PRLICANTON NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-037-417-46 (1-357) x US-09-386-642-9 (1-1049)
                                                                                                                                                                            Mismatches:
                                                                                                                                                                                           Indels:
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                   LIBRARY: COLNNOT27
CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
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100.00%
3.64%
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100.00%
100.00%
3.64%
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     IMMEDIATE SOURCE:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                      US-09-008-271A-19
                                                                                                        Alignment Scores:
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US-09-386-642-9
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                                                                                                                                                                                            Query Match:
DB:
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                                                                                                                            Pred. No.:
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STEVEN D.
NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Nucleotide sequence encoding Tumor Antigen Derived OTHER INFORMATION: Gene-14 (TADG-14) protein; nt 1344-1360 NCBI accession OTHER INFORMATION: #AA343629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REPERENCE: D6020CIPP CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1360
13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys 249
                                                                                                                                                                                                                                                                                                                         213 GACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGT 175
                                                                                                                                                                                                                                                                                           237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys 249
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
; OTHER INFORMATION: Anti-sense sequence of TADG-14 US-09-618-259-72
                                                                                                                                                                                                                                                  US-10-037-417-46 (1-357) x US-09-618-259-72 (1-1343)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: .72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COHEN, MAURICE
APPLICANT: COLFITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: KLASS, MICHAEL N.
APPLICANT: RUSSELL, OORN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/09618259 ; Patent No. 6642013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-944-483-5; Application US/08944483
; Sequence 5. Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
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100.00%
100.00%
3.64%
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13.00
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US-09-280-116-29/c

US-09-280-116-29/c

Sequence 29, Application US/09280116A

Sequence 29, Application US/09280116A

Sequence 29, Application

Sequence 29, Application

Sequence 29, Application

Sequence 29, Application

Reith E.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/280,116A

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 268

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grieve, Robert B.
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 1990
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340
111
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     10000
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Conservative:
Mismatches:
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: trypsin-like serine proteases
                                                                                                                                                                     250 CAGGGAGATTCTGGGGGGCCCCTGGTCTGTGAA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GlnGlyAspSerGlyGlyProLeuValCysGlu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 CAGGGAGATTCTGGGGGCCCCTGGTCTGTGAA 218
                                                                                                                                                240 GlnGlyAspSerGlyGlyProLeuValCysGlu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-037-417-46 (1-357) x US-09-280-116-29 (1-340)
                                                                                                             US-10-037-417-46 (1-357) x US-09-280-116-28 (1-340)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                     Indels:
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100.00%
100.00%
3.08%
 11.00
100.00%
100.00%
3.08%
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ORGANISM: Homo sapiens
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CITY: Denver
STATE: Colorado
COUNTRY: USA
               Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-906-769-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: U$/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 receasestratices description 102
                                                                                                                                                                                                                     OPERATING SYSTEM: DOS.
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-037-417-46 (1-357) x US-08-944-483-5 (1-262)
TITLE OF INVENTION: OF THE PROSTATE NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park CITY: Abbott Park COUNTX: USA
ZITY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6183.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09280116A Patent No. 6331427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Becker, Cheryl L.
REGIENATION NUMBER: 35,441
REFRENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEFAX: 847/938-2623
                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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11.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-280-116-28/c
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US-08-944-483-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
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/note= "At pos. bp 301, change A to W; at pos. bp 397, change C to W; at pos. bp 342, change C to Y; at pos. bp 331, change G to S. At pos. aa 100, 114 and 144, substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 122, Application US/08639075A
; Sequence 122, Application US/08639075A
; Patent No. 6150125
; GENERAL INFORMATION:
   APPLICANT: Grieve, Robert B.
   APPLICANT: Rushlow, Keith E.
   APPLICANT: Rushlow, Keith E.
   APPLICANT: Strenk, Glann R.
   APPLICANT: Strenk Glann R.
   APPLICANT: Strenk Glann R.
   APPLICANT: Gaines, Patrick J.
   APPLICANT: Gaines, Patrick J.
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   APPLICANT: Gaines, Patrick J.
   APPLICANT: Gaine
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MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-ARR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: COMPALI, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 GACACTTGCCAGGGAGATTCAGGTGGGCCATTG 289
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Indels:
CLASSIFICATION: 536
ATTOWNEY/ABENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/EDOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LEMOTH: 436 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNES: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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100.00%
100.00%
3.08%
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LOCATION: 2..436
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE;
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Query Match:
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CITY: Denver
STATE: Colorad
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US-08-639-075A-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-906-616-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "At pos. bp 301, change A to
W; at pos. bp 342, change C to Y; at pos. bp 397, change C to
at pos. bp 431, change G to S. At pos. aa 100, 114 and 144,
substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/906,616 FILING DATE: 05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-037-417-46 (1-357) x US-08-906-769-122 (1-436)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 GACACTTGCCAGGGAGATTCAGGTGGGCCATTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/639,075
FILING DATE: 24-AR-1996
ATTORNEY,AGENT INFORMATION:
NAME: Connell, Gary J., REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26.18-25-C2
TELECHONE: (303) 863-9700
TELECHONE: (303) 863-9700
TELECHONE: (303) 863-9700
TELECHONE: (303) 863-9700
TELECHONE: (303) 863-9700
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TELECHONE: (303) 863-9700
TELECHONE: (303) 863-9700
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05-AUG-1997
      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheridan Ross P.C.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.00
100.00%
100.00%
3.08%
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LOCATION: 2..436
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1700 Linc
CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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incorporation: 2..436

incorporation: 2..436

orher information: /note= "At pos. bp 301, change A to

what pos. bp 342, change C to Y; at pos. bp 397, change C to Y;

at pos. bp 431, change G to S. At pos. as 100, 114 and 144,

substitute Xaa.;

sequence bescription: SEQ ID NO: 122:

US-09-012-431-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09032215
Patent No. 6204010
GENERAL INFORMATION:
APPLICANT: Stiegler, Gary L.
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLAB PROTEASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF NUMBER OF SEQUENCES: 50
CORRESPONDENCE Sheridan Ross P.C.
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-037-417-46 (1-357) x US-09-012-431-122 (1-436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 AspThrCysGlnGlyAspSerGlyGlyProLeu 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 GACACTTGCCAGGGAGATTCAGGTGGGCCATTG 289
                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: FLORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ASCIT DOS TEXT
CURRENT APPLICATION DATA:
FILING DATE: 27-FEB-1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 27-FEB-1998
CLASSIFICATION DATA:
FRIGHTON NUMBER:
FILING DATE:
ATTORNPV'ANTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
TELEFAX: (303) 863-0223
               INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 mucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                         11.00
100.00%
100.00%
3.08%
                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 8020A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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US-09-032-215-19
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W; at pos. bp 342, change C to Y; at pos. bp 397, change C to
at pos. bp 431, change G to S. At pos. aa 100, 114 and 144,
substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 80203

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRNT APPLICATION DATA:

APPLICATION NUMBER: US/09/012,431

FILING DATE: 23-Jan-1998

CLASSIFICATION: <Unknown>
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ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-037-417-46 (1-357) x US-08-639-075A-122 (1-436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AspThrCysGlnGlyAspSerGlyGlyProLeu 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 GACACTIGCCAGGGAGATICAGGIGGGCCATIG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
Stiegler, Gary
Gaines, Patrick J.
Silver, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 122, Application US/09012431; Patent No. 6180383; GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 190
                      TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 122
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           0.0669
11.00
100.00%
100.00%
                                                                                                          LENGTH: 436 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                         LOCATION: 2..436
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
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Matches:
Conservative:
Mismatches:
Capp:
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                                                                                                                                                                                                                                                         Score: 0.0669
Score: 11.00
Percent Similarity: 100.008
Best Local Similarity: 100.008
Ouery Match: 3.088
| TOPOLOGY: linear | MOLECULE TYPE: CDNA | FRAURE: | NAME/KEY: CDS | LOCATION: 1..436 | LOCATION: 1..436 | LOCATION: 301 | LOCATION: 301 | FRAURE: | NAME/KEY: Y = C | LOCATION: 342, 397 | FRAURE: | NAME/KEY: S = C | LOCATION: 431 | FRAURE: | NAME/KEY: S = C | LOCATION: 431 | FRAURE: | NAME/KEY: Xaa = Unknown | LOCATION: 100, 114, 1444 | US-09-032-215-19
                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
Score:
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Search completed: February 26, 2004, 00:08:19 Job time : 101 secs

g

protein

Run on:

Sequence: Title: Perfect :

Word size: Searched:

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              Sequence 10, Appl
Sequence 21306, A
Sequence 7606, Appl
Sequence 29, Appl
Sequence 85, Appl
Sequence 11, Appl
Sequence 141, Appl
Sequence 2214, Appl
Sequence 261, Appl
Sequence 261, Appl
Sequence 261, Appl
Sequence 271, Appl
Sequence 271, Appl
Sequence 271, Appl
Sequence 271, Appl
Sequence 271, Appl
Sequence 271, Appl
              US-10-221-097-10
US-10-221-097-10
US-10-029-386-7606
US-10-042-865-31
US-10-042-865-29
US-10-176-847-85
US-09-980-107-2214
US-09-967-768A-141
                                                                                                                                                                                                                 # US-10-097-340-261

# US-10-097-340-261

# US-10-101-510-441

# US-10-101-510-621

# US-10-101-510-621

# US-10-101-510-621

# US-09-978-295A-394

# US-09-978-697-394

# US-09-978-192A-394

# US-09-978-182A-394

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APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REPERBNCE: 038602/1214
CURRENT APPLICATION NUMBER: 10S/09/888,615
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOPTWARE: Patentin Ver: 2.1
SEQ ID NO 52
TURNET 2457
TURNET 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 52, Application US/0988615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
TYPE: DNA ORGANISM: Homo sapiens
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-MODEL=frame+ p.D.:.model -DEV=xlp
-MODEL=frame+ p.D.:.model -DEV=xlp
-Q=/CgnZ 1/USPTO spool p/US10037417/runat_24022004_101110_18195/app_query.fasta_1.519
-Q=/CgnZ 1/USPTO spool p/US10037417/runat_24022004_101110_18195/app_query.fasta_1.519
-DS=Published Applications NA -OFMT=fastap -SUFFIX=olip2n.rnpb -MINMATCH=0.1
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-LOOPCI=0 -LOOPEXT=0 -UNITS=bits -STRRT=1 -END=-1 -MATRIX=oligo
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-RGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                                      February 25, 2004, 23:28:21; Search time 399 Seconds (without alignments) 3133.050 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                              1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications NA:*

| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                             Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Database :

US-09-888-615-52

Description

Score

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277
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                                                                                                                                                                                                                                                                                                                                                                                  137
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                                                                                                                                         TGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCCCTCATC 231
                                                                                                                                                                                                                                                                                         291
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                                                                                                                                                                                                 TrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySerLeuIle 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr
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                                        Conservative:
Mismatches:
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            Length:
Matches:
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US-10-221-097-10
Sequence 10, Application US/10221097
Publication No. US20030144476A1
GENERAL INFORMATION:
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272.00
100.00%
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                                Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
Pred. No.:
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Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR TITLE OF INVENTION: BAPPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001_12_20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 21306
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OTHER INFORMATION: MAP TO CHRI6.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9
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Conservative:
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APPLICANT: Murdock, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Santh, Randall F.
APPLICANT: Santh, Randall F.
APPLICANT: Santh, Randall F.
APPLICANT: Santh, Randall F.
APPLICANT: Santh, Randall F.
APPLICANT: Santh, Randall F.
FILE REFRENCE: GPSOOLS
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: CT/USO1/07143
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PSEGSEQ FOR WINDOWS Version 3.0
SERVITANE: 768
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US-10-221-097-10
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Best Local Similarity:
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; APPLICANT: Agarwal, Pankaj

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APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polymucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 2140-2.537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
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16
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Mismatches:
Indels:
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Matches:
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PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR PELLING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-8
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
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                                      Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei '
Gangolli, Esha A
Burgess, Catherine E
                                                                                                                                                                                                                                                                         Guo, Xiaojia
Boldog, Ference In
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie I
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
MacDougall, John
Mallet, Isabelle
Peyman, John
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APPLICANT: Li, Li
APPLICANT: Zerhußen, Bryan D
                                                                                                                                                                                                                                   Tchernev, Velizar T
Miller, Charles E
                                                                                                                                                                                     Vernet, Corine A.M
Taylor, Sarah
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Gunther, Erik
                    Zerhusen, Bryan D
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SEQ ID NO 31
LENGTH: 1161
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ORGANISM: Homo sapiens
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Pred. No.:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, DAVID R.
APPLICANT: HANZEL, DAVID R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SSQ ID NO 7606
LENGTH: 543
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: EXTREMENCH HIT: Q16651, EVALUE 7.00e+00
OTHER INFORMATION: BST HUMAN HIT: AU142128.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: U33446.1, EVALUE 0.00e+00
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADDUT LIVER, SIGNAL = 3.6
OTHER INFORMATION: NT HIT: Gil4719472, EVALUE 0.000+40
OTHER INFORMATION: SWISSPROT HIT: Q16651, EVALUE 1.000-08
OTHER INFORMATION: EST_HUMAN HIT: AU142128.1, EVALUE 0.000+00
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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                                                                                                                                                                            Length:
Matches:
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Sequence 7606, Application US/10029386
Polication No. US20030194704A1
GENERAL INFORMATION:
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16.00
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Pred. No.:
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US-10-042-865-31
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US-09-948-094-1

Sequence 1, Application US/09948094

Sequence 1, Application US/09948094

Sequence 1, Application US/09948094

Sequence 1, Application US-09625A1

GENERAL INFORMATION:

APPLICANT: The Brigham and Women's Hospital, Inc.

APPLICANT: Mok, Samuel

APPLICANT: Wong, Kwong-Kwok

TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin

FILLE REPRESENCE: 81994/28323

CIRRENT APPLICATION NUMBER: US/09/948,094

CURRENT PILING DATE: 2001-09-07
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APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
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Mismatches:
Indels:
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Matches:
Conservative:
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Matches:
CURRENT APPLICATION NUMBER: US/10/176,847 CURRENT FILING DATE: 2002-06-21 NUMBER OF SEQ ID NOS: 112 SOFTWARE: EastSEQ for Windows Version 4.0 SEQ ID NO 85 LENGTH: 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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SOFTWARE: Patentin version 3.0
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LOCATION: (229)..(1260)
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CRGANISM: Homo sapiens
US-10-176-847-85
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LENGTH: 1834
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Publication No. US20030068636A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
TITLE OF INVENTION: AND OVARIAN CANCER
FILE REFERENCE: MRI-039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stone, David

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/42,865
CURRENT FILING DATE: 2002-05-17
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR PRILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
SPRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PATENTING WINDER: 60/284,704
PRIOR FILING DATE: 2001-04-18
SOFTWARE: PATENTING NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
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Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
                                                                                                                                                                                                                                                                                                                                                                                               Taylor, Valizar Taylor, Valizar Taylor, Xaojia Boldog, Ference Larosse, William Malsobrook II, John Perlach, Valerie Ledinger, Shlomit R Rothenberg, Mark E Blerman, Karen MacDougall, John Malyankar, Uriel Millet, Isabelle Peyman, John
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Gunther, Erik
                              Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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) ORGANISM: Homo sapiens
US-10-042-865-29
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Pred. No.:
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Query Match:

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APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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TITLE OF INVENTION: Mucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Mucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
NUMBER OF SEQ ID NOS: 363
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US-10-101-510-447

Sequence 447, Application US/10101510

Publication No. US20030148295A1

GENERAL INFORMATION:

APPLICANT: WAN, JACKSON

TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE

FILE REFERENCE: 15117.0012

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: 60/276,947

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 805

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 447
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John MONAHAN
Manjula GANNAVARAPU
Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel B. MEYERS
Michael MORRISEY
Peter OLANDT
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Robert C. BAST, Jr.
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Xumei ZHAO
Karen GLATT
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                                                                                                                                                                                                                                          Karen LU
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Sequence 141, Application US/09967768A

Patent No. US2002015087A1

GENERAL INFORMATION:

APPLICANT: Adjustue, Meena

TITLE OF INVENTION: Sets

FILLE REFERENCE: 689230-72

CURRENT APPLICATION NUMBER: US/09/967,768A

CURRENT APPLICATION NUMBER: US/60/236,109

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

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PRIOR FILING DATE: 2000-09-28

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PRIOR FILING DATE: 2000-09-28

SEQ ID NO 141

LENGTH: 1834
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Matches:
Conservative:
Mismatches:
Indels:
    CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-66-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOUTHARE: PatentIn Ver. 2.1
LENGTH: 1834
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ORGANISM: Homo sapiens
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US-10-097-340-261
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Sequence 3, Application US/10325745

Sequence 3, Application US/10325745

Publication No. US20030135028A1

GENERAL INFORMATION:

APPLICANT: NI et al.

ITILE OF INVENTION: Human Serine Protease and Serpin Polypeptides

FILE REFERENCE: PF391D1

CURRENT APPLICATION WUMBER: US/10/325,745

CURRENT APPLICATION NUMBER: US 09/244,111

PRIOR APPLICATION NUMBER: US 60/073,961

PRIOR FILING DATE: 1999-02-06

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 792
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US-10-101-510-621
Sequence 621, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION PROFILES AND FILING DATE: 2002-03-20
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT PILING DATE: 2002-03-20
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
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NAME/KEY: CDS

LOCATION: (85)..(708)

OTHER INFORMATION:
US-10-325-745-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-447
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US-10-325-745-3
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Sequence 612, Application US/10101510
; Sequence 612, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
APPLICANT: WANG, YIXIN
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REPERBENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR PILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 612
; LENGTH: 994
; TYPE: DNA
; ORGANISM: HOMO Sapiens
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Conservative:
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Matches:
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Mismatches:
Indels:
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Job time : 406 secs
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3.64%
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; TENGTH: 988
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; ORCANISM: Homo sapiens
US-10-101-510-621
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US-10-101-510-612
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VERSION
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Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

Contier Korean EST Project 2001

Unpublished (2002)
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K-EST0101694 S9SNU601 Homo sapiens cDNA clone S9SNU601-51-E07 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
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ESULT 6

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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llh.gov/bbrp/Aimage/Aimage.html
Insert Length: 691 Std Error: 0.00
Seq primer: -400P from Gibco
Seq primer: -400P from Gibco
High quality sequence stop: 334.
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A1393077 360 bp mENA linear EST 30-MAR-1999 tq25£08.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109831 3' similar to SW:PSSS HUMAN Q16651 PROSTASIN PRECURSOR ; mRNA
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1 (bases 1 to 360)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP cancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index (1997)
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/clone="IMAGE:2109831"
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6.1%; Score 67; DB 9; Length 360;
Best Local Similarity. 100.0%; Pred. No. 1.9e-20;
Matches 67; Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
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EST.
Homo sapiens (human)
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

CE 1 (bases 1 to 294)

RS Adams,M.D. Kralavage,A.R.; Fleischmann,R.D.; Fuldner,R.A.;

Bult,C.J.; Lee,N.H.; Kirkness,E.F.; Weinstock, K.G.; Gocayne,J.D.;

White,O.; Sutton,G.; Blake,J.A.; Brandon,R.C.; Man.Wai,C.;

Clayton,R.A.; Cline,T.R.; Cotton,M.D.; Earle-Hughes,J.; Fine,L.D.;

Fitzgerald,L.M.; Fitzhugh,W.M.; Fritchman,J.L.; Geoghagen,N.S.;

Glodek,A.; Gnehm,C.L.; Hanna,M.C.; Hedblow,E.; Hinkle,P.S.Jr.;

Kelley,J.A.; Kelley,J.C.; Liu,L.I.; Marmaros,S.M.; Merrick,J.M.;

Moreno-Palanques,R.F.; McDonald,L.A.; Nayen,D.T.; Pelligrino,S.M.;

Phillips,C.A.; Ryder,S.E.; Scott,J.L.; Saudek,D.M.; Shirley,R.;

Small,K.V.; Spriggs,T.A.; Utterback,T.R.; Weidman,J.F.; Li,Y.;

Bednarik,D.P.; Cao,L.; Cepeda,M.A.; Coleman,T.A.; Collins,E.J.;

Dinke,D.; Reng,D.-F.; Rernie,A.; Fischer,C.; Hastings,G.A.;

Kozak,D.L.; Kunsch,C.; Hungjun,J.; Li,H.; Weissner,P.S.; Olsen,H.;

Raymond,L.; Wei,Y.F.; Wing,J.; Xu,C.; Yu,G.L.; Ruben,S.M.;

Praser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Un Nature 377 (6547 Suppl), 3-174 (1995)
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Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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/note="Organ: uterus; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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6.1%; Score 67; DB 9; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 67; Conservative 0; Mismatches 0; Indels
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226 AAGACCCAGTCAGAT 240
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BP 191 91006 EVRY cedex - France
Librairy was constructed by Life Pechnologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7995.f For
Invitrogen. This sequence belongs to sequence cluster 7995.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact
Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP001AD09FM1.
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                                                                                                                                                                                                                                                                   84 CAGATATTGCCAGGGAIGCTGTGTGTGTGCTACCCAGAGGCCGCAGGGACACCTGCCAG 25
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 930)
                                            204 GTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAAGTGGAAGTTAAAGGCTG
     559 GICCAGGAGGCAGAICCICIGCCICICCCCTGGGTGCTACAGGAAGIGGAGCTAAGGCTG
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Pred. No. 1.4e-52;
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Homo sapiens
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BX436299

ACCESSION VERSION KEYWORDS

DEFINITION

RESULT 3 BX436299

SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

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Gaps

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Matches 135;

811

Query Match

ORIGIN

166 871

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